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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2001, 16:43:01 ; Search time 26.57 Seconds
(without alignments)
178.884 Million cell updates/sec

Title: US-09-203-768a-2

Perfect score: 748
Sequence: 1 MKHLWPELLVAAPRWVLSQ.....ARPHRYPDYWGCGTLTVSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_36: *
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT: *
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT: *
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT: *
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT: *
5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT: *
6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT: *
7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT: *
8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT: *
9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT: *
10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT: *
11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT: *
12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT: *
13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT: *
14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT: *
15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT: *
16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT: *
17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT: *
18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT: *
19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT: *
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT: *
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	83.2	116	16	Human immunoglobulin
2	588	78.6	139	21	Human PTHrP monocl
3	580	77.5	139	21	Human 5' EST relat
4	575.5	76.9	472	17	Anti-Thesius D reco
5	566	75.7	244	20	Amino acid sequenc
6	560.5	74.9	136	18	Immunoglobulin rB6
7	558.5	74.7	123	17	Anti-thesius D mono
8	558.5	74.7	142	14	FI05 rearranged va
9	552	73.8	128	12	Anti-human RHD FOM
10	550	73.5	116	14	Vh 71-4. Homo sap
11	550	73.5	116	16	Human immunoglobul
12	543	72.6	141	21	Amino acid sequenc

13	541.5	72.4	476	18	W01822
14	541.5	72.4	476	19	W63765
15	539.5	72.1	470	21	Y44721
16	539	72.1	118	16	R66348
17	539	72.1	475	17	R93553
18	538	71.9	116	16	R66298
19	536.5	71.7	140	18	W32477
20	536.5	71.7	140	19	W43430
21	536.5	71.7	140	21	Y56732
22	536.5	71.7	141	14	R31948
23	536.5	71.7	467	18	W14927
24	536.5	71.7	467	18	W14925
25	536.5	71.7	467	18	W14926
26	536	71.7	139	21	Y56713
27	536	71.7	141	19	W70378
28	532.5	71.2	139	18	W35284
29	532.5	71.2	139	18	W14932
30	532.5	71.2	139	19	W53988
31	532.5	71.2	143	21	Y56706
32	530.5	70.9	134	15	R54049
33	530.5	70.9	134	17	W01526
34	530.5	70.9	134	18	W24986
35	530	70.9	140	21	W64689
36	529.5	70.8	121	12	R12270
37	529.5	70.8	476	18	W01818
38	529.5	70.8	476	19	W63761
39	527	70.5	118	16	R66329
40	527	70.5	125	9	P81259
41	526.5	70.4	139	19	W57446
42	526.5	70.4	155	21	Y64727
43	521	69.7	118	16	R66342
44	517	69.1	205	20	Y34299
45	516.5	69.1	117	21	Y68899

ALIGNMENTS

RESULT 1	
R66324	R66324 standard; Protein: 116 AA.
XX	
AC	R66324;
XX	
DT	03-AUG-1995 (first entry)
XX	
DE	Human immunoglobulin variable heavy chain #30.
XX	
KW	Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW	cosmid; placenta; vector; pUB81; E.coli; mammalian.
XX	
OS	Homo sapiens.
XX	
PN	W09426895-A.
XX	
PD	24-NOV-1994.
XX	
PF	10-MAY-1993; 93WO-JP00603.
XX	
PR	10-MAY-1993; 93WO-JP00603.
XX	
PA	(NISR) JAPAN TOBACCO INC.
XX	
PI	Honjo T, Matsuda F;
XX	
DR	WPI: 1995-006791/01.
XX	
DR	N-PSDB: Q78972.
XX	
PT	DNA fragment comprising human immunoglobulin Vh genes - for the
PT	production of human immunoglobulin in mammalian hosts
XX	
PS	Claim 41; Page 74-75; 130pp; Japanese.
XX	

CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
 CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were
 CC isolated and cloned from a series of cosmid constructs: Y102; Y103; Y21;
 CC Y6724; 3-31; M84; M118 and M131, by PCR amplification using primers
 CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
 CC fragments cover a region of 800 kb. The DNA fragments were isolated from
 CC high molecular weight DNA from human placenta. The DNA was partially
 CC digested with TaqI restriction enzyme. The fragments were separated by
 CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
 CC were ligated with ClaI-digested cosmid vector pUB1. The ligation
 CC products were in vitro packed and infected into E. coli 490A. The
 CC fragments were then subcloned by colony hybridisation. The Vh genes and
 CC the DNA fragments encoding them are useful in producing human
 CC immunoglobulin in mammalian hosts.

CC Sequence 116 AA:

Query Match 83.2%; Score 622; DB 16; Length 116;
 Best Local Similarity 100.0%; Pred. No. 8.5e-45;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKNLWFFLLVAAPRWVLSQVLOQWAGLKPSETLSLTCAVYGGSFSGYWSWIRPP 60
 DB 1 mkhlwfflllvaaprwlvsqvgqlkpsetlsltcavysgysywswirpp 60
 OY 61 GKGLEWIGELINHSSTNYPNLSKSRVTISVDTSKNOFSLKLSVTADPAAVYCAEIA 116
 DB 61 gkglewlgelnhsstnypnlsksrvtisvdtksnqfslklsvtaadpavycar 116

RESULT 2
 Y82628
 ID Y82628 standard; Protein: 139 AA.

AC Y82628;
 DT 02-AUG-2000 (first entry)

DE Human PTHrP monoclonal antibody clone 4B4-6-21 protein SEQ ID NO:40.

KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingivitis;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antihypertensive; cyclostatic; antineoplastic.

OS Homo sapiens.

Key Location/Qualifiers
 FH Misc-difference 77
 FT /note="possibly Tyr"

PN JP2000080100-A.

PD 21-MAR-2000.

PE 12-OCT-1998; 98JP-0304793.

PR 17-JUN-1998; 98JP-0188196.

PR 26-JUN-1998; 98JP-0196729.

PA (NIBS) JAPAN TOBACCO INC.

DR WPI: 2000-286723/25.

DR N-PSDB; A13938.

PT A human monoclonal antibody to parathyroid hormone related protein.
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain

PS Claim 32; Page 75; 88pp; Japanese.

CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antihypertensive, cyclostatic and
 CC antineoplastic activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone protein sequence from the
 CC present invention.

CC Sequence 139 AA:

Query Match 78.6%; Score 588; DB 21; Length 139;
 Best Local Similarity 82.0%; Pred. No. 6.5e-42;
 Matches 114; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

OY 1 MKNLWFFLLVAAPRWVLSQVLOQWAGLKPSETLSLTCAVYGGSFSGYWSWIRPP 60
 DB 1 mkhlwfflllvaaprwlvsqvgqlkpsetlsltcavysgysywswirpp 60
 OY 61 GKGLEWIGELINHSSTNYPNLSKSRVTISVDTSKNOFSLKLSVTADPAAVYCAEIA 120
 DB 61 gkglewlgelnhsstnypnlsksrvtisvdtksnqfslklsvtaadpavycar 120
 OY 121 RPHRYFDYWGOGCTLTWVSS 139
 DB 121 yyygldwvgggtltvss 139

RESULT 3
 Y64676
 ID Y64676 standard; Protein: 139 AA.

AC Y64676;

DT 01-FEB-2000 (first entry)

DE Human 5' EST related polypeptide SEQ ID NO:837.

KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
 KW gene therapy; chromosome mapping; upstream regulatory sequence;
 KW forensic; location; development; protein synthesis; stability;
 KW regulation; identification.

OS Homo sapiens.

PN W09953051-A2.

PD 21-OCT-1999.

PE 09-APR-1999; 99WO-1B00712.

PR 09-APR-1998; 98US-0057719.

PR 28-APR-1996; 98US-0069047.

PA (GENET) GENSET.

PI Dumas Mline Edwards J, Duclert A, Giordano J;

DR WPI: 2000-038446/03.

DR N-PSDB; Z42290.

PT Novel secreted protein 5' expressed sequence tag sequences used in
 PT diagnostic, forensic, gene therapy, and chromosome mapping procedures
 PT including metastasis, and pain

PS Claim 3; Page 605-606; 837pp; English.

XX Z42265 to Z43075 represent novel 5' expressed sequence tag (EST)

PR	03-DEC-1997;	97US-0067428.	
XX			
PA	(BOE) BOEHRINGER MANNHEIM CORP.		
PI	Mahoney W, Sawyer JR, Winter GP;		
XX			
DR	WPI: 1999-432068/37.		
XX	N-PSDB: X86940.		
PT	New anti-complex antibody useful for diagnosing prostate cancer		
XX			
PS	Claim 28; Page 25-27; 42pp: English.		
XX			
CC	The invention relates to an antibody that binds a complex between		
CC	prostate-specific antigen (PSA) and anti-chymotrypsin (ACT), and has an		
CC	affinity for the complex which is at least 10 fold higher than the		
CC	affinity for either PSA or ACT alone. The antibody is used in diagnostic		
CC	assays to detect PSA-ACT in serum samples from patients. The levels of		
CC	PSA-ACT complex increase in patients suffering from prostate cancer		
CC	compared to the levels in patients with benign or no growths in the		
CC	prostate. Therefore detection of PSA in complex with ACT is useful for		
CC	the early detection of prostate tumours, by distinguishing between benign		
CC	and malignant conditions of the prostate as well as for the management		
CC	of patients with prostate cancer, such as the disclosure of metastasis and		
CC	the monitoring of the PSA levels after treatment. The antibodies may		
CC	also be used in immunotherapy, affinity chromatography and isolation or		
CC	purification of PSA-ACT. Unlike prior art antibodies which bind to		
CC	PSA-ACT complexes but may also bind PSA or ACT alone, the present		
CC	antibody is specific for PSA-ACT alone. Diagnostic assays using the		
CC	antibodies are more accurate in diagnosing prostate cancer as they only		
CC	detect the intact complex of PSA-ACT. Sequences Y21880-884 represent		
CC	specific examples of antibodies directed against PSA-ACT. The present		
CC	sequence represents the amino acid sequence of antibody BIOA8.		
XX			
SQ	Sequence	244 AA:	
	Query Match	75.7%;	Score 566; DB 20; Length 244;
	Best Local Similarity	89.3%;	Pred. No. 7.6e-40;
	Matches 109; Conservative	5;	Mismatches 4; Indels 4; Gaps 1
OY	18 LSOVLOOMGALLRPSERLSITCAVYGGSEFGYVSMIRPPGKLEWIGELNHGSGTN 77		
	:::		
DB	1 maevqlgeagagllkpselstlscavyygsifsgyyswtirppgkylewlgelnsgstn 60		
OY	78 YNPSLKSRVTIIVDSKKNQFSLKLSVTADPAVYYCAREIARPHRYEDYMGQGLTVY 137		
DB	61 ynpslksrvtlsvdlsknqfslklsstvtadavyycaarmwslk----fdyggqgcltvcv 116		
OY	138 SS 139		
DB	117 ss 118		
RESULT	6		
ID	W24536		
XX	W24536 standard; Protein; 136 AA.		
AC	W24536;		
XX			
DT	09-OCT-1997 (first entry)		
XX			
DE	Immunoglobulin RB6B7 heavy chain variable region.		
XX			
KW	Immunoglobulin; variable region; heavy chain; thyrotropin receptor;		
KM	thyroid stimulating activity; light chain; Basedow's disease; antibody;		
XX	peripheral blood lymphocyte.		
OS	Homo sapiens.		
XX			
TH	Key	Location/Qualifiers	
PT	Peptide	1..19	

```

FT      Protein                               /note="signal peptide"
FT      JP09140386-A.                        20.136
XX
XX      03-JUN-1997.
XX
XX      22-NOV-1995;    95JP-0328235.
XX
XX      22-NOV-1995;    95JP-0328235.
XX
XX      (EIKE ) EIKEN KAGAKU KK.
XX
XX      WPI: 1997-344899/32.
XX      DR      N-PSDB: T79919.
XX
XX      Antibody containing immunoglobulin heavy chain mutation - with
XX      thyroid function stimulating activity
XX
XX      Claim 31; Page 14-15; 18pp; Japanese.
XX
XX      W24536-W24539 represent the immunoglobulin heavy and light chain variable
XX      regions isolated from peripheral blood lymphocyte strains. These
XX      sequences were isolated from the B6B7 and 101-2 strains of peripheral
XX      blood lymphocytes of a Basedow's disease patient. These sequences are
XX      replaced, deleted or inserted into an antibody, to create the antibodies
XX      of the invention. The antibodies of the invention have thyroid function
XX      stimulating activity, and act by combining with thyrotropin receptor. The
XX      antibody can be used in a method to detect autoantibodies which have
XX      thyroid function stimulating activity.
XX
XX      Sequence 136 AA;
SQ

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```

Query Match Similarity      74.9%; Score 560.5; DB 18; Length 136;
Best Local Similarity      81.6%; Pred. No. 1,2e-39;
Matches 111; Conservative 4; Mismatches 18; Indels 3; Gaps 2

QY      1 MKHLWFEELLVAAPRKVLSQVQLQQWAGCLLKPSEFLSLTCAVYGGSGFSGYWMTIRPP 60
        |||||
Db       1 mkhlwfeellvaaprkvlsqvqlqgesgpplvpseclstlctvsgsissgywswlrpp 60
        |||||

QY      61 GKGLEWIGEINHSQSTNINYPSLKSRVTISVDTSKNOFSLKLSVTAADRAVYICAREI-- 118
        |||||
Db       61 gkglewigyihysgstnynsslskrvtlsvdtsknfslklsstvadtaavycareerg 120
        |||||

QY      119 AARPHRY-FDYWGOGGF 133
        |||||
Db       121 glrdflaygmddwvqgl 136

RESULT  7
W03757
ID       W03757 standard; Protein: 123 AA.
AC       W03757;
XX
XX
DT       29-OCT-1996 (first entry)
XX
XX
DE       Anti-rhesus D monoclonal antibody D7C2 heavy chain V region.
XX
XX
KW       Human monoclonal antibody; immunoglobulin isotype Igm; agglutination;
KW       rhesus positive; rhesus negative; haemolysis; heavy chain;
KW       variable region; insect host cell; baculovirus; recombinant production.
XX
XX
OS       Homo sapiens.
XX
XX
Key      Location/Qualifiers
FT       Region                29..35
FT       /label= CDR1
FT       /note= "complementarity determining region"
FT       50..65
FT       /label= CDR2
FT       Region

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FT	Region	/note= "complementarity determining region"
FT		98.112
FT		/label= CDR3
FT		/note= "complementarity determining region"
PN	FR724182-A1.	
XX		
PD	08-MAR-1996.	
XX		
PF	02-SEP-1994;	94FR-0010566.
XX		
PR	02-SEP-1994;	94FR-0010566.
XX		
PA	(INSP) INST PASTEUR.	
PA	(PROT-) PROTEINE PERFORMANCE.	
XX		
PI	Chaabih H, Edelman L, Kaczorek M, Margaritte C;	
XX		
DR	WPI: 1996-162018/17.	
DR	N-PSDB; T26870.	
XX		
PT	Recombinant anti-rhesus D monoclonal antibody - expressed by baculovirus-transformed insect cells and useful for preventing haemolysis in new-born babies	
PT		
XX		
PS	Example 1; Page 32; 46pp; French.	
XX		
CC	The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in new-born rhesus positive babies.	
CC	Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of the variable region of the IgM-D7C2 heavy chain.	
CC		
XX		
XX	Sequence 123 AA;	

Query Match	74.7%	Score 558.5	DB 17	Length 123
Best Local Similarity	78.6%	Pred No. 1.6e-39		
Matches 109	Conservative 3	Mismatches 8	Indels	Gaps 3
QY	20	QVQLDQMGAGLLKPSSETLSLTCAVYGGSGFYWMSNIROP	PKGLEWIGELINHSSTNN	79
Db	1	qyqlgwgagllkpssetlslctctygsfsygywswlrqp	pgkglewigeinhsstnn	60
QY	80	PSLKRRLVTSVDTSNNOESLKLSSVTAAFTAYYYCAR--	EIAARPH-RREDVWGQCTLT	136
Db	61	pslksrvlsvdtsknqslslklnsvtaadtavycarapek	kwkynghdwfdpwwgqtlvt	120
QY	137	VSS	139	
Db	121	VSS	123	
RESULT	8			
ID	R41285			
AC	R41285			
DT	01-NOV-1993	(first entry)		
DE	F105	rearranged variable region heavy chain.		
KW	Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;			
KM	Cys; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;			
XX	chain; epitope; immune deficiency.			
XX	Homo sapiens.			

FH	Key	Location/Qualifiers
FT	Peptide	1..19
FT	/label= sig-peptide	
FT	Protein	20..142
FT	/label= mat.protein	
XX		
PN	W09J312232-A.	
XX		
PD	24-JUN-1993.	
XX		
FF	10-DEC-1992;	92MO-US10928.
XX		
PR	10-DEC-1991;	91US-0804652.
PA	(DAND) DANA FARBER CANCER INST INC.	
PA	(NEME-) NEW ENGLAND DEACONNESS HOSPITAL CORP.	
PI	Haseltine WA, Marasco WA, Posner MR, Sodroski JG;	
XX		
DR	WPI; 1993-214174/26.	
DR	N-PSDB; Q49154.	
XX		
PT	DNA segments encoding monoclonal antibody - which binds to gp120	
PT	and neutralises HIV, for treating AIDs, and for diagnosing and	
PT	monitoring HIV infection	
XX		
PS	Claim 9-10; Page 77; 109pp; English.	
XX		
CC	mRNA from the known hybridoma F105 was converted to cDNA and this	
CC	subjected to PCR amplification using primers corresp. to appropriate	
CC	pats of the heavy or light chains and having restriction sites to	
CC	permit cloning. The extension prods. were isolated and sequenced.	
CC	The recombinant human monoclonal antibody (Mab) binds to a	
CC	discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks	
CC	the binding of gp120 to the CD4 receptor, and neutralises a broad	
CC	range of HIV isolates. The Mab may be used to treat immune	
-CC	deficiency, esp. at doses of 0.1-10 mg/Kg.	
S0	Sequence 142 AA:	

[illegible]

FH Key Location/Qualifiers
 FT Region 31..35 /label= CDR1
 FT Region 50..65 /label= CDR2
 FT Region 98..117 /label= CDR3
 FT Region /label= CDR3
 PN WO9107492-A.
 XX 30-MAY-1991.
 PD 13-NOV-1990; 90MO-BP01964.
 XX 13-NOV-1989; 89GB-0025590.
 PR 13-NOV-1989; 89GB-0025590.
 XX (BLOO-) CENT BLOOD LAB AUTH.
 PA Hughes - Jones N;
 PI WPI: 1991-178104/24.
 DR N-PSDB; Q11951.
 XX
 PT DNA encoding complementary determining regions - of human
 PT anti-rhesus D antibodies, useful in Prodn. of monoclonal
 PT antibodies and for passive immunisation
 PS Disclosure: Fig 8; 32pp; English.
 CC The DNA sequence of eleven monoclonal antibodies are
 CC represented in Q119145-57. Synthetic genes, for both heavy and
 CC light chains may be created by combining selected CDR 1, 2, and 3
 CC regions, which may be selected from different antibody mols. having
 CC varied binding specificity. The chimeric anti-Rhd antibodies can be
 CC used for diagnosis and therapy, and are capable of providing blood-
 CC typing reagents of high specificity and reliability. They can also
 CC be used in passive immunisation to prevent haemolytic disease of the
 CC newborn.
 CC
 XX
 SQ Sequence 128 AA:

Query Match 73.8%; Score 552; DB 12; Length 128;
 Best Local Similarity 83.7%; Pred. No. 5.7e-39;
 Matches 108; Conservative 4; Mismatches 7; Indels 10; Gaps 2;

QY 20 QYQLOOMGAGLKPSETLSLTCAYVGGSGFYWMIRPPKGLGEWIGEINHSSTNN 79
 DB 1 qvqlqwgagllkpselstlcaavgssstgywmwlrppkgglewlgelhsstnyn 60
 QY 80 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCARETIAARPHR-----YFDYWG 130
 DB 61 pslkrsrvtsvdtksknqfslkssvtaadtaavycargl-erplnqllnrlgyymdwvg 119
 QY 131 OGTELVTVSS 139
 DB 120 kgtvtvss 128

RESULT 10
 R42689 R42689 standard; Protein; 116 AA.
 AC R42689;
 DT 01-NOV-1993 (first entry)
 DE Vh 71-4.
 XX Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CDR; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency.
 XX

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19 /label= sig_peptide
 FT Protein 20..116 /label= mat_protein
 FT Region 49..54 /label= CDR1
 FT Region 69..84 /label= CDR2
 FT Region /label= CDR2
 PN WO9312232-A.
 XX 24-JUN-1993.
 PD 10-DEC-1992; 92MO-US10928.
 XX 10-DEC-1992; 92MO-US10928.
 PF 10-DEC-1991; 91US-0804652.
 PR 10-DEC-1991; 91US-0804652.
 XX (DAND) DANA FARBER CANCER INST INC.
 PA (NEWME-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 XX Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
 PI WPI: 1993-214174/26.
 DR N-PSDB; Q42697.
 XX
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Disclosure: Page 64; 109pp; English.
 CC The nucleotide sequence of rearranged F105 Vh (Q42698) was compared
 CC to two monoclonal antibodies (Ab26 - Q42702) and 268-D - Q42703),
 CC which by nucleotide sequence analysis, appear to use a rearranged
 CC Vh 71-4 gene (Q42697).
 CC Ab26 (Q42702) was derived from CD5+ B cells of a healthy donor and
 CC represents a naturally occurring polyclonal antibody which binds to
 CC many antigens. Ab26 shares greatest sequence similarity with germline
 CC Vh 71-4.
 CC
 XX
 SQ Sequence 116 AA:

Query Match 73.5%; Score 550; DB 14; Length 116;
 Best Local Similarity 90.5%; Pred. No. 7.5e-39;
 Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKHMFELLVAAPRWVLSOVLOOMGAGLKPSETLSLTCAYVGGSGFYWMIRPP 60
 DB 1 mkhlwfflllvaaprwvlsqvqlqgsqplvkrpselstlcvsgsvssywmwlrpp 60
 QY 61 GKLEWIGEINHSSTNNPSLSKSRVTISVDTSKNQFSLKSSVTAADTAVYYCAR 116
 DB 61 gkglewlgelhsstnynpslsksrvtsvdtksknqfslkssvtaadtaavycar 116

RESULT 11
 R66346 R66346 standard; Protein; 116 AA.
 AC R66346;
 DT 04-AUG-1995 (first entry)
 DE Human immunoglobulin variable heavy chain #52.
 XX
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJ881; E.coli; mammalian.
 XX Homo sapiens.
 OS

PA (IDEC-) IDEC PHARM CORP.
 XX
 XX
 PI Anderson DR, Brams P, Hanna N, Shestowsky WS;
 XX
 DR WPI: 1997-108638/10.
 DR N-PSDB: T62513.
 XX
 PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen
 XX useful for treating autoimmune disease or graft-versus-host disease
 PS Claim 14; Fig 10B; 81pp; English.
 XX
 CC 2 Polypeptides (W01821 and W01822) respectively comprise primate
 CC forms of the light and heavy chains of cynomolgus monkey anti-human
 CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
 CC heavy variable genes (see also T62512 and T62513) are inserted into
 CC an expression vector (pref. NEOSPIA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of the primate
 CC antibody in e.g. CHO cells. Primatized 7C10 and 7B6 anti-B7.1
 CC antibodies have also been produced (see also W01817-20). The
 CC primate antibodies inhibit the B7/CD28 pathway, making them
 CC useful immunosuppressants for the treatment of autoimmune disorders
 CC and graft-versus-host disease.
 CC
 XX Sequence 476 AA;
 SQ
 Query Match 72.4%; Score 541.5; DB 18; Length 476;
 Best Local Similarity 74.0%; Pred. No. 1.6e-37;
 Matches 108; Conservative 11; Mismatches 20; Indels 7; Gaps 3;
 QY 1 MKHLMEFLLLVAPRWVLSQVOLDQWAGLLKPSFTLSLTCAVYGSFS-GYVMSWIRP 59
 DB 1 mhlhlfllllvaprwlvsqvdqesgplvpselstlcavsgsisgygwygtrp 60
 QY 60 PKGLGWIGET-NHSGSTNYNPSLSKRVITISVTSKNQPSLSKLSVTADTAAYVCARE- 117
 DB 61 pklglwlgfsfyssgntlynpiskqvylstcdskngfsiklnmtlaedavycvdr 120
 QY 118 ----IAARHRYEDWGGSTLVTYSS 139
 DB 121 lfsvgywnwfdwpgvplvtvss 146
 RESULT 14
 W63765
 ID W63765 standard; Protein: 476 AA.
 XX
 AC W63765;
 XX
 DT 29-SEP-1998 (first entry)
 XX
 DE Macaque primate 16C10 heavy chain protein.
 XX
 KW Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation.
 XX
 OS Macaca fascicularis.
 XX
 PN W09819706-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 29-OCT-1997; 97WO-US19906.
 XX
 PR 08-NOV-1996; 96US-0746361.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Brams P, Hanna N;

XX
 DR WPI: 1998-286601/25.
 DR N-PSDB: V35489.
 XX
 PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 XX inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 XX cells, e.g. graft rejection or tumours
 PS Example 7; Fig 5b; 87pp; English.
 XX
 CC This sequence represents a primate form of the antibody 16C10 heavy
 CC chain from macaque. This sequence is used in a method studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 CC
 XX Sequence 476 AA;
 SQ
 Query Match 72.4%; Score 541.5; DB 19; Length 476;
 Best Local Similarity 74.0%; Pred. No. 1.6e-37;
 Matches 108; Conservative 11; Mismatches 20; Indels 7; Gaps 3;
 QY 1 MKHLMEFLLLVAPRWVLSQVOLDQWAGLLKPSFTLSLTCAVYGSFS-GYVMSWIRP 59
 DB 1 mhlhlfllllvaprwlvsqvdqesgplvpselstlcavsgsisgygwygtrp 60
 QY 60 PKGLGWIGET-NHSGSTNYNPSLSKRVITISVTSKNQPSLSKLSVTADTAAYVCARE- 117
 DB 61 pklglwlgfsfyssgntlynpiskqvylstcdskngfsiklnmtlaedavycvdr 120
 QY 118 ----IAARHRYEDWGGSTLVTYSS 139
 DB 121 lfsvgywnwfdwpgvplvtvss 146
 RESULT 15
 Y44721
 ID Y44721 standard; Protein: 470 AA.
 XX
 AC Y44721;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human immune system molecule, ISMO-2.
 XX
 KW Human; immune system molecule; ISMO-2; incyte clone 2849752; diagnosis;
 KW treatment; prevention; cell proliferation; immune system disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Signal_peptide
 FT Protein 20..470
 FT /label= Mature_ISMO-2
 FT Modified-site 120
 FT /note= "N-glycosylated"
 FT Modified-site 320

FT	Modified-site	/note= "N-glycosylated"
FT	105	
FT	/note= "Casein kinase II phosphorylation site"	
FT	232	
FT	Modified-site	
FT	290	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	
FT	377	/note= "Casein kinase II phosphorylation site"
FT	47	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	
FT	81	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	
FT	92	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	
FT	98	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	
FT	142	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	
FT	154	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	
FT	322	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	
FT	347	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	
FT	460	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	
FT	69	/note= "Tyrosine kinase phosphorylation site"
FT	Modified-site	
FT	319	/note= "Tyrosine kinase phosphorylation site"
FT	Modified-site	
FT	Region	
FT	387..409	/note= "Tyrosine kinase phosphorylation site"
FT	Region	
FT	446..463	/note= "conserved Ig/MHC protein block"
FT	Domain	
FT	34..116	/note= "conserved Ig/MHC protein block"
FT	domain	
FT	160..225	/note= "shows similarity to Ig superfamily protein domain"
FT	Domain	
FT	160..225	/note= "shows similarity to Ig superfamily protein domain"
FT	Domain	
FT	383..450	/note= "shows similarity to Ig superfamily protein domain"
FT	Domain	
FT	160..225	/note= "shows similarity to Ig superfamily protein domain"
XX	WO20000608-A2.	
PN	06-JAN-2000.	
PD	06-JAN-2000.	
XX	21-JUN-1999;	99WO-US13995.
PE	21-JUN-1999;	99WO-US13995.
XX	30-JUN-1998;	98US-0107223.
PR	30-JUN-1998;	98US-0107223.
XX	(INCY-) INCYTE PHARM INC.	
PA	(INCY-) INCYTE PHARM INC.	
PI	Lal P, Tang YT, Corley NC, Gorgone G, Guegler KU, Patterson C;	
P1	Baughn MR:	
XX	WPI: 2000-170916/15.	
DR	N-PADB: Z50012.	
DR	N-PADB: Z50012.	
XX	Immun system molecules used in the diagnosis, treatment and prevention	
PT	of disorders associated with the immune system and cell proliferation	
PT	-	
PS	Claim 1; Pages 60-61; 69pp; English.	
XX	The present sequence is an immun system molecule,	
CC	ISMO-2 from an Incyte clone 2849752 isolated from the human breast	
CC	tumour cDNA library (BSTRV13). This sequence is expressed in several	
'CC	libraries, generally those associated with cancer, cell	
CC	proliferation, immun response or trauma. It shows homology to	
CC	vertebrate immunoglobulin gamma heavy-chain.	

CC The present sequence is useful in the diagnosis, treatment and
CC prevention of disorders associated with the immune system and
CC cell proliferation.
XX
SQ Sequence 470 AA;

Fri Mar 9 16:49:01 2001

us-09-203-768a-2.rag

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: March 9, 2001, 16:43:01 ; Search time 23.59 Seconds
(without alignments)
400.093 Million cell updates/sec

Title: US-09-203-768a-2

Perfect score: 748

Sequence: 1 MKHLWFFLLVAPRWVLSQ.....ARPHRYFDYWGQGLTVVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	685.5	91.6	140	2 A49045	Ig heavy chain V r
2	641	85.7	140	2 S78052	Ig heavy chain pre
3	625.5	83.6	140	2 I37782	Ig variable region
4	589	78.7	139	2 S31586	Ig heavy chain V r
5	585	78.2	137	2 S31676	Ig heavy chain V r
6	584.5	78.1	147	2 S13519	Ig heavy chain V r
7	576	77.0	145	2 S78055	Ig heavy chain pre
8	571.5	76.4	146	1 G1H012	Ig heavy chain pre
9	571	76.3	126	2 S47010	Ig heavy chain V4.
10	570.5	76.3	139	2 S31506	Ig heavy chain V r
11	569.5	76.1	155	2 S31511	Ig heavy chain - h
12	563.5	75.3	155	2 S31512	Ig heavy chain - h
13	560.5	74.9	146	2 S09711	Ig heavy chain V r
14	558	74.6	231	2 B23746	Ig Fab region IV-J
15	554.5	74.1	143	2 B49028	Ig heavy chain V-I
16	550	73.5	116	2 B26340	Ig heavy chain pre
17	544.5	72.8	146	2 S09710	Ig heavy chain V r
18	539	72.1	118	2 A26340	Ig heavy chain pre
19	538	71.9	116	2 S18557	Ig heavy chain V r
20	535.5	71.6	140	2 A24770	Ig heavy chain V r
21	530.5	70.9	130	2 S31690	Ig heavy chain V r
22	530	70.9	122	2 J10047	Ig heavy chain V r
23	519	69.4	139	2 A41287	Ig heavy chain pre
24	518	69.3	124	2 S26898	Ig heavy chain V r
25	518	69.3	124	2 S31684	Ig heavy chain V r
26	514.5	68.8	114	2 I72667	cold agglutinin FS
27	514.5	68.8	130	2 S31673	Ig heavy chain V r
28	512.5	68.5	135	2 S78051	Ig heavy chain pre
29	512	68.4	143	2 B41287	Ig heavy chain pre

30	509	68.0	97	2 S14474	Ig heavy chain V r
31	508.5	68.0	137	2 S31585	Ig heavy chain V r
32	508	67.9	97	2 G34964	Ig heavy chain V-I
33	497.5	66.5	117	2 B34964	Ig heavy chain pre
34	490	65.5	97	2 S26805	Ig heavy chain V r
35	488	65.2	135	2 S31604	Ig heavy chain V r
36	483	64.6	97	2 S26806	Ig heavy chain V r
37	483	64.6	97	2 JH0428	Ig gamma chain V r
38	475	63.5	129	2 S44114	Ig heavy chain V r
39	472	63.1	97	2 S26808	Ig heavy chain V r
40	472	63.1	130	2 S30534	Ig heavy chain V r
41	466.5	62.4	121	2 S44113	Ig heavy chain V r
42	466	62.3	118	2 S24443	Ig heavy chain V r
43	464.5	62.0	123	2 S30530	Ig heavy chain V r
44	464	62.0	120	2 P30370	Ig mu chain precu
45	463.5	62.0	127	2 S19668	Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49045
R:Grillot-Courvalin, C.; Broquet, J.C.; Piller, F.; Rasseint, L.Z.; Labaume, S.; Silve
Eur. J. Immunol. 22, 1781-1788, 1992
A>Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes 1
A:Reference number: A49045; MUID:92324290
A:Accession: A49045
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <GR>
A:Cross-references: GB:S39381; NID:q250899; PID:AA622441.1; PID:q250900
A>Note: sequence extracted from NCBI backbone (NCBI:108088, NCBI:P:108089)
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IM>

Query Match 91.6%; Score 685.5; DB 2; Length 140;
Best Local Similarity 94.3%; Pred. No. 1.1e-54;
Matches 132; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

OY 1 MKHLWFFLLVAPRWVLSQVLOQWAGLLKPSFTLSITCAVYGSGFYWSMIRPP 60
    |||
Db 1 MKHLWFFLLVAPRWVLSQVLOQWAGLLKPSFTLSITCAVYGSGFYWSMIRPP 60

OY 61 GKGLMEIGINHSSTNYPNPSLSKSVTTSVDTSKNOFSLSKTSVTAADTAVYYCAR-EIA 119
    |||
Db 61 GKGLMEIGINHSSTNYPNPSLSKSVTTSVDTSKNOFSLSKTSVTAADTAVYYCAR-GRA 120

OY 120 ARPHRYFDYWGQGLTVVSS 139
    |
Db 121 ATIVESFDYWGQGLTVVSS 140

RESULT 2
S78052
Ig heavy chain precursor V-D-J region (clone mab 63VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78052; S23717
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78052
A:Molecule type: mRNA
A:Residues: 1-140 <HAR>
A:Cross-references: EMBL:X54441; NID:q37815; PID:CAA38308.1; PID:q930118
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notk
```

Int. Immunol. 3, 865-875, 1991
 A>Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h patient.
 A:Reference number: S23716; MUID:92031262
 A:Accession: S23717
 A:Molecule type: mRNA
 A:Residues: 15-111 <HAW>
 A:Cross-references: EMBL:X54441
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: Immunoglobulin
 F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
 F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAN>
 F:29-111/Domain: immunoglobulin homology <IMM>

Query Match 85.7%; Score 641; DB 2; Length 140;
 Best Local Similarity 88.7%; Pred. No. 1.1e-50;
 Matches 126; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

OY 6 FLLVAPRWVLSQVLOQMGAGLKPSETLSITCAVYGSGFSGYWMIROPPKGL 65
 DB 1 KHLVAPRWVLSQVLOQMGAGLKPSETLSITCAVYGSGFSGYWMIROPPKGL 60
 OY 66 WIGELNHSGSTNPNPILSKSRVTISVDTSKNPFSLKSSVTADTAVYYCAR-----E 117
 DB 61 WIGELNHSGSTNPNPILSKSRVTISVDTSKNPFSLKSSVTADTAVYYCARGGSVLRLE 120
 OY 118 IAPRHRYFDYWGQGLTVTVSS 139
 DB 121 WLLYP--AFDYWGQGLTVTVSS 140

RESULT 3

Ig variable region (VDJ) (clone T23-9) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
 C:Accession: J37782; S25476
 R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
 A>Title: Somatic diversification in the heavy chain variable region genes expressed by
 A:Reference number: A6876; MUID:94119917
 A:Accession: J37782
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-140 <RES>
 A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA46104.1; PID:g33583
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 625.5; DB 2; Length 140;
 Best Local Similarity 86.4%; Pred. No. 2.6e-49;
 Matches 121; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

OY 1 KHLVAPRWVLSQVLOQMGAGLKPSETLSITCAVYGSGFSGYWMIROPP 60
 DB 1 KHLVAPRWVLSQVLOQMGAGLKPSETLSITCAVYGSGFSGYWMIROPP 60
 OY 61 GKLEWIGELNHSGSTNPNPILSKSRVTISVDTSKNPFSLKSSVTADTAVYYCAR 120
 DB 61 GKLEWIGELNHSGSTNPNPILSKSRVTISVDTSKNPFSLKSSVTADTAVYYCARHNS 120
 OY 121 RPHY--FDYWGQGLTVTVSS 139
 DB 121 SWYGRYFDYWGQGLTVTVSS 140

RESULT 4

S31586
 Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31586
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
 A:Reference number: S31585
 A:Accession: S31586
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-139 <CU>
 A:Cross-references: EMBL:Z14182; NID:g30978; PIDN:CAA76565.1; PID:g30979
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 589; DB 2; Length 139;
 Best Local Similarity 82.9%; Pred. No. 4.9e-46;
 Matches 115; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

OY 1 KHLVAPRWVLSQVLOQMGAGLKPSETLSITCAVYGSGFSGYWMIROPP 60
 DB 1 KHLVAPRWVLSQVLOQMGAGLKPSETLSITCAVYGSGFSGYWMIROPP 60
 OY 61 GKLEWIGELNHSGSTNPNPILSKSRVTISVDTSKNPFSLKSSVTADTAVYYCAR 120
 DB 61 GKLEWIGELNHSGSTNPNPILSKSRVTISVDTSKNPFSLKSSVTADTAVYYCARGLG 120
 OY 121 RPHRYFDYWGQGLTVTVSS 139
 DB 121 IRRGAFDIDWGQGLTVTVSS 139

RESULT 5

Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31676
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
 A:Reference number: S31585
 A:Accession: S31676
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-137 <CU>
 A:Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA76551.1; PID:g31032
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 585; DB 2; Length 137;
 Best Local Similarity 82.9%; Pred. No. 1.1e-45;
 Matches 116; Conservative 4; Mismatches 16; Indels 4; Gaps 2;

OY 1 KHLVAPRWVLSQVLOQMGAGLKPSETLSITCAVYGSGFSGYWMIROPP 60
 DB 1 KHLVAPRWVLSQVLOQMGAGLKPSETLSITCAVYGSGFSGYWMIROPP 60
 OY 61 GKLEWIGELNHSGSTNPNPILSKSRVTISVDTSKNPFSLKSSVTADTAVYYCAR 120
 DB 61 GKLEWIGELNHSGSTNPNPILSKSRVTISVDTSKNPFSLKSSVTADTAVYYCAR 117
 OY 121 RPHRY--FDYWGQGLTVTVSS 139
 DB 118 APLMYGMDYWGQGLTVTVSS 137

RESULT 6

S13519
 Ig heavy chain V region precursor - human
 C:Species: Homo sapiens (man)

C>Date: 25-Feb-1994 #sequence-revision 10-Nov-1995 #text-change 23-Jul-1999
 C/Accession: S13519
 R/Mottari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
 Nucleic Acids Res. 19, 673, 1991
 A>Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
 A/Reference number: S13519; MUID:91187691
 A/Accession: S13519
 A>Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-147 <MOR>
 A/Cross-references: EMBL:X56158; NID:q37724; PIDN:CAA39626.1; PID:q37725
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotetramer; Immunoglobulin
 F:41-125/Domain: Immunoglobulin homology <IMM>

Query Match 78.1%; Score 584.5; DB 2; Length 147;
 Best Local Similarity 82.3%; Pred. No. 1.3e-45;
 Matches 116; Conservative 5; Mismatches 17; Indels 3; Gaps 2;

OY 1 MKHLWFLLVAAPRWVLSQVQLQOMGAGLLKPSSETLSLTCAVYGGSF--SGYWSMIROP 58
 |||||
 DB 8 MKHLWFLLVAAPRWVLSQVQLQOMGAGLLKPSSETLSLTCAVYGGSSSSSYWGMIRQ 67
 OY 59 PGKGLWIEIINHGSGTNNPISLKRVTISVDTSKNPSLKLSSVTAADTAVYYCAREI 118
 |||||
 DB 68 PGKGLWIEIINHGSGTNNPISLKRVTISVDTSKNPSLKLSSVTAADTAVYYCARPL 127
 OY 119 AARPHRYFDYWGQGLTVTVSS 139
 |||||
 DB 128 LWF-GEIIFDYWGQGLTVTVSS 147

RESULT 7

S78055
 Ig heavy chain precursor V-D-J region (clone MAB 67VH) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 19-Nov-1997 #sequence-revision 05-Dec-1997 #text-change 23-Jul-1999
 C/Accession: S78055; S23720
 R/Harindranath, N.
 Submitted to the EMBL Data Library, August 1990
 A/Reference number: S78051
 A/Accession: S78055
 A/Molecule type: mRNA
 A/Residues: 1-145 <HAR>
 A/Cross-references: EMBL:X54445; NID:q37817; PIDN:CAA38312.1; PID:q37818
 R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
 Int. Immunol. 3, 865-875, 1991
 A>Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and H
 patient.
 A/Reference number: S23716; MUID:92031262
 A/Accession: S23720
 A/Molecule type: mRNA
 A/Residues: 18-115 <HAR>
 A/Cross-references: EMBL:X54445
 A/Note: the authors translated the codon GCA for residue 67 as Arg
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: Immunoglobulin
 F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
 F:18-145/Product: Ig heavy chain (fragment) #status predicted <MAR>
 F:32-115/Domain: Immunoglobulin homology <IMM>

Query Match 77.0%; Score 576; DB 2; Length 145;
 Best Local Similarity 79.5%; Pred. No. 7.5e-45;
 Matches 116; Conservative 6; Mismatches 14; Indels 10; Gaps 3;

OY 3 HLMFELLVAAPRWVLSQVQLQOMGAGLLKPSSETLSLTCAVYGGSF--SGYWSMIROP 61
 |||||
 DB 1 HLMFELLVAAPRWVLSQVQLQOMGAGLLKPSSETLSLTCAVYGGSSSSSYWGMIRQ 60
 OY 62 KLEWTEIINHGSGTNNPISLKRVTISVDTSKNPSLKLSSVTAADTAVYYCARLAA- 120
 |||||

DB 61 KLEWTEIINHGSGTNNPISLKRVTISVDTSKNPSLKLSSVTAADTAVYYCARVGTST 120
 OY 121 -----RPHRYFDYWGQGLTVTVSS 139
 |||||
 DB 121 FMSGYTRGT-YFDYWGQGLTVTVSS 145

RESULT 8

GIH082
 Ig heavy chain precursor V-II region (ARH-77) - human
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1987 #sequence-revision 30-Jun-1987 #text-change 02-Sep-1997
 C/Accession: A02101
 R/Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
 Gene 33, 181-189, 1985
 A>Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat se
 A/Reference number: A02101; MUID:85205332
 A/Accession: A02101
 A/Molecule type: mRNA
 A/Residues: 1-146 <KUD>
 A/Note: the sequence was determined from the differentiated gene
 A/Note: the authors translated the codon GGC for residue 17 as Arg
 C/Genetics:
 A/Gene: GDB:IGHV6
 A/Cross-references: GDB:128528; OMIM:147070
 A/Map position: 14q32.33-14q32.33
 A/Introns: 16/3
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotetramer; Immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <MAR>
 F:20-117/Region: V segment
 F:35-117/Region: Immunoglobulin homology <IMM>
 F:118-127/Region: D segment
 F:128-146/Region: J segment
 F:42-115/Disulfide bonds: #status predicted

Query Match 76.4%; Score 571.5; DB 1; Length 146;
 Best Local Similarity 78.1%; Pred. No. 1.9e-44;
 Matches 114; Conservative 5; Mismatches 20; Indels 7; Gaps 2;

OY 1 MKHLWFLLVAAPRWVLSQVQLQOMGAGLLKPSSETLSLTCAVYGGSSSGYWSMIROP 59
 |||||
 DB 1 MKHLWFLLMCQLPDVGLVLSQVQLQOMGAGLLKPSSETLSLTCAVFGSGSYWMIROP 60
 OY 60 PGKGLWIEIINHGSGTNNPISLKRVTISVDTSKNPSLKLSSVTAADTAVYYCARLAA 119
 |||||
 DB 61 PGKGLWIEIINHGSGTNNPISLKRVTISLPTSKNLFSLKLSSVTAADTAVYYCARGLL 120
 OY 120 AARPHRYFDY-----WGQGLTVTVSS 139
 |||||
 DB 121 RGMNDVVDYRYGMDVWGQGLTVTVSS 146

RESULT 9

S47010
 Ig heavy chain V4.21-UniqueD-J5 region - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence-revision 13-Jan-1995 #text-change 23-Jul-1999
 C/Accession: S47010
 R/Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
 submitted to the EMBL Data Library, July 1994
 A/Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody
 A/Reference number: S47009
 A/Accession: S47010
 A/Molecule type: mRNA
 A/Residues: 1-126 <MAH>
 A/Cross-references: EMBL:Z35492; NID:q517254; PIDN:CAA84626.1; PID:q517255
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotetramer; Immunoglobulin
 F:15-97/Domain: Immunoglobulin homology <IMM>

Query Match 76.3%; Score 571; DB 2; Length 126;
 Best Local Similarity 87.3%; Pred. No. 1.8e-44;
 Matches 110; Conservative 3; Mismatches 7; Indels 6; Gaps 1;

OY 20 OVLOQMGAGLLKPSFTLSLTCAVYGGSFSGYWSWIRPPGKLEWIGELINHSSTNN 79
 |||||
 DB 1 OVLOQMGAGLLKPSFTLSLTCAVYGGSFSGYWSWIRPPGKLEWIGELINHSSTNN 60
 |||||
 OY 80 PSLKSVTISVDTSKNOFSLKSVTAADTAAYYCAR-----ETARPHRYFDYGGGT 133
 |||||
 DB 61 PSLKSVTISVDTSKNOFSLKSVTAADTAAYYCARGGCCPKKACCYTKNMFDPWGGGT 120
 |||||
 OY 134 LVTYSS 139
 |||||
 DB 121 LVTYSS 126

RESULT 10

S31696

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31696
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelier, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A:Reference number: S31585
 A:Accession: S31696
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-139 <CU>
 A:Cross-references: EMBL:Z14194; NID:g30975; PIDN:CAA8563.1; PID:g30976
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 570.5; DB 2; Length 139;
 Best Local Similarity 81.5%; Pred. No. 2.2e-44;
 Matches 110; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

OY 1 MKHLWFLLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCAVYGGSFSGYWSWIRPP 60
 |||||
 DB 1 MKHLWFLLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCTVSGSISYWSWIRPPA 60
 |||||
 OY 61 GKLEWIGELINHSSTNNPISLKSRYTISVDTSKNOFSLKSVTAADTAAYYCAR-EIA 119
 |||||
 DB 61 AGKLEWIGITRYSGSTNNPISLKSRYTISVDTSKNOFSLKSVTAADTAAYYCARGGIG 120
 |||||
 OY 120 AARPHRYFDYGGGT 134
 ::|||
 DB 121 LMGDKWIDWGGGT 135

RESULT 11

S31511

Ig heavy chain - human

C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S31511
 R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
 submitted to the EMBL Data Library, December 1992
 A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
 A:Reference number: S31509
 A:Accession: S31511
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-155 <CH>
 A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 569.5; DB 2; Length 155;
 Best Local Similarity 77.8%; Pred. No. 3.1e-44;
 Matches 112; Conservative 7; Mismatches 18; Indels 7; Gaps 2;

OY 1 MKHLWFLLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCAVYGGSFSGYWSWIRPP 60
 |||||
 DB 14 MKHLWFLLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCTVSGSISYWSWIRPP 73
 |||||
 OY 61 GKLEWIGELINHSSTNNPISLKSRYTISVDTSKNOFSLKSVTAADTAAYYCAR-EIA 120
 |||||
 DB 74 GKLEWIGITRYSGSTNNPISLKSRYTISVDTSKNOFSLKSVTAADTAAYYCAR--CG 131
 |||||
 OY 121 AARPHRYFDYGGGT 139
 ::|||
 DB 132 GISSWYDYGMVDWGGGT 155

RESULT 12

S31512

Ig heavy chain - human

C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S31512
 R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
 submitted to the EMBL Data Library, December 1992
 A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA a
 A:Reference number: S31509
 A:Accession: S31512
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-155 <CH>
 A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 563.5; DB 2; Length 155;
 Best Local Similarity 78.9%; Pred. No. 1.1e-43;
 Matches 112; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

OY 1 MKHLWFLLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCAVYGGSFSGYWSWIRPP 60
 |||||
 DB 14 MKHLWFLLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCTVSGSISYWSWIRPP 73
 |||||
 OY 61 GKLEWIGELINHSSTNNPISLKSRYTISVDTSKNOFSLKSVTAADTAAYYCAR--EI 118
 |||||
 DB 74 GKLEWIGITRYSGSTNNPISLKSRYTISVDTSKNOFSLKSVTAADTAAYYCARGGGI 133
 |||||
 OY 119 AARPHRYFDYGGGT 139
 ::|||
 DB 134 SSWYDYGMVDWGGGT 155

RESULT 13

S09711

Ig heavy chain V region - human

C:Species: Homo sapiens (man)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 C:Accession: S09711
 R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coatswell, J.
 Biochem. J. 268, 135-140, 1990
 A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domain
 A:Reference number: S09710; MUID:90262535
 A:Accession: S09711
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-146 <HUG>
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

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OM protein - protein search, using sw model

Run on: March 9, 2001, 16:43:06 ; Search time 14.74 Seconds
(without alignments)
304.537 Million cell updates/sec

Title: US-09-203-768a-2

Perfect score: 748
Sequence: 1 MKHLMFLLVAAAPRWLSQ.....ARPHRYFDYWGQGLTVYSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571.5	76.4	146	1	HV21_HUMAN
2	411.5	55.0	129	1	HV2F_HUMAN
3	408	54.5	137	1	HV46_MOUSE
4	397.5	53.1	117	1	HV2G_HUMAN
5	370	49.5	116	1	HV60_MOUSE
6	369.5	49.4	144	1	HV43_MOUSE
7	359.5	48.1	113	1	HV47_MOUSE
8	359.5	48.1	135	1	HV02_XENLA
9	343	45.9	116	1	HV61_MOUSE
10	330	44.1	139	1	HV07_MOUSE
11	329	44.0	137	1	HV11_MOUSE
12	328	43.9	119	1	HV37_MOUSE
13	326.5	43.6	117	1	HV62_MOUSE
14	326	43.6	119	1	HV38_MOUSE
15	325	43.4	119	1	HV40_MOUSE
16	323.5	43.2	138	1	HV48_MOUSE
17	322	43.0	122	1	HV3G_HUMAN
18	321	42.9	136	1	HV01_XENLA
19	317.5	42.4	117	1	HV41_MOUSE
20	316.5	42.3	118	1	HV33_MOUSE
21	316.5	42.3	142	1	HV01_RAT
22	316	42.2	115	1	HV50_MOUSE
23	310	41.4	120	1	HV50_MOUSE
24	306.5	41.0	123	1	HV22_MOUSE
25	305.5	40.8	121	1	HV01_MOUSE
26	304	40.6	116	1	HV45_MOUSE
27	303.5	40.6	115	1	HV3B_HUMAN
28	303.5	40.6	117	1	HV42_MOUSE
29	302.5	40.4	117	1	HV13_MOUSE
30	302.5	40.4	140	1	HV02_MOUSE
31	300.5	40.2	117	1	HV12_MOUSE
32	300.5	40.2	121	1	HV3J_HUMAN
33	299	40.0	147	1	HV2H_HUMAN

34	297	39.7	120	1	HV2B_HUMAN
35	296	39.6	118	1	HV51_MOUSE
36	295.5	39.5	120	1	HV03_MOUSE
37	295.5	39.5	123	1	HV18_MOUSE
38	295.5	39.5	123	1	HV19_MOUSE
39	294.5	39.4	123	1	HV23_MOUSE
40	293	39.2	122	1	HV3H_HUMAN
41	292.5	39.1	119	1	HV2C_HUMAN
42	290.5	38.8	117	1	HV04_MOUSE
43	288.5	38.6	117	1	HV17_MOUSE
44	288	38.5	122	1	HV20_MOUSE
45	287.5	38.4	116	1	HV36_MOUSE

ALIGNMENTS

RESULT	ID	Query Match	Score	DB 1	Length
HV21_HUMAN	1	76.4%	571.5	DB 1	146
HV21_HUMAN	1	Best local Similarity	78.1%	Pred. No. 1e-47	
AC	P06331	Matches 114; Conservative	5;	Mismatches 20;	Indels 7;
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG HEAVY CHAIN V-II REGION ARH-77 PRECURSOR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=85205332; PubMed=3922855;				
RX	Kudo A., Ishihara T., Nishimura Y., Watanabe T.;				
RT	"A cloned human immunoglobulin heavy chain gene with a novel direct-				
RT	repeat sequence in 5' flanking region."				
RL	Gene 33:181-189(1985).				
DR	PIR; A02101; G1H042.				
DR	HSSP; P01825; 7FAB.				
DR	INTERPRO; IPR003006; .				
DR	PFAM; PF00047; Ig; 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL	1	19		
FT	CHAIN	20	146		
FT	DOMAIN	20	117		
FT	DOMAIN	118	127		
FT	DOMAIN	128	146		
FT	DISULFID	142	115		
FT	NON_TER	146	146		
SQ	SEQUENCE	146 AA; 16228 MW; 8D7FD52BB218171F CRC64;			
Query Match		76.4%	Score 571.5; DB 1; Length 146;		
Best local Similarity		78.1%; Pred. No. 1e-47;			
Matches 114; Conservative		5;	Mismatches 20;	Indels 7;	Gaps. 2;
QY	1	MKHLMFLLVAAAPRWLSQVQLQIQAGLRLPSELTSTCAVYGGSGYYWSWIRP	59		
DB	1	MKHLMFLLVAAAPRWLSQVQLQIQAGLRLPSELTSTCAVYGGSGYYWSWIRP	60		
QY	60	PKGLEWIGELINSGSNYNPSLKSRTISVDTSKNQPSLKSSTVTAADAVYCAEIA	119		
DB	61	PKGLEWIGELINSGSNYNPSLKSRTISVDTSKNQPSLKSSTVTAADAVYCAEIA	120		
QY	120	ARPHRYFDY-----WGQGLTVYSS 139			
DB	121	RGGMNDVDYTYGMDVWGQGLTVYSS 146			
RESULT	2				
HV2F_HUMAN		STANDARD;	PRT;	129 AA.	
HV2F_HUMAN					
AC	P01824;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				

DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE IG HEAVY CHAIN V-II REGION WAH.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE:
 RX MEDLINE=8222235; PubMed=6806818;
 RA Takahashi N., Teteart D., Debuire B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 immunoglobulin D."; Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 RL -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 CC PROTEIN.
 DR PIR: A02099; D2HUMA.
 DR HSSP: P01825; 7FAB.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 DR IMMUNOGLOBULIN V region.
 FT NON_TER 129 129
 FT SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 55.0%; Score 411.5; DB 1; Length 129;
 Best Local Similarity 62.1%; Pred. No. 1.4e-32;
 Matches 82; Conservative 14; Mismatches 21; Indels 15; Gaps 3;

QY 20 QVQLQOQWAGLTKRPSFLSLTCAVYGGSF--SGYWSMIRPPKGLGEMGELNHSSTN 77
 DB 1 RLQLQSGPEGLVPSFLSLTCAVSGGPIRRGTGYWGMIPGPKGLGEMGELNHSSTN 60
 QY 78 YNPSLRVTISVDTSKNPSFLSLTCAVYGGSF--SGYWSMIRPPKGLGEMGELNHSSTN 127
 DB 61 YNPSLRVTISVDTSKNPSFLSLTCAVYGGSF--SGYWSMIRPPKGLGEMGELNHSSTN 117
 QY 128 YWGQGLTVTVSS 139
 DB 118 YWGQGLTVTVSS 129

RESULT 3

HV46_MOUSE STANDARD; PRT; 137 AA.
 ID HV46_MOUSE
 AC P01822;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1992 (Rel. 23, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE IG HEAVY CHAIN V REGION MOPC 315 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89238351; PubMed=2497341;
 RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
 RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
 gene segment."; Mol. Immunol. 26:431-434(1989).
 RL [2]
 RN [2]
 RP SEQUENCE OF 1-31.
 RX MEDLINE=78094475; PubMed=414225;
 RA Jilka R.L., Pestka S.;
 RT "Amino acid sequence of the precursor region of MOPC-315 mouse
 immunoglobulin heavy chain."; Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
 RN [3]
 RP SEQUENCE OF 1-21.
 RX MEDLINE=79148758; PubMed=428562;
 RA Schechter I., Wolf O., Zemel R., Burstein Y.;
 RT "Structure and function of immunoglobulin genes and precursors."; Fed. Proc. 38:1833-1845(1979).
 RL [4]
 RN [4]
 RP SEQUENCE OF 19-136.

RX MEDLINE=74170779; PubMed=4524622;
 RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;
 RT "Amino acid sequence of the variable region of the heavy (alpha)
 chain of a mouse myeloma protein with anti-hapten activity."; Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
 RN [5]
 RP REVISION TO 53.
 RX MEDLINE=77244979; PubMed=268248;
 RA Hood L., Margolies M.N., Givol D., Zakut R.;
 RL Unpublished results, cited by:
 RL Padan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
 RL -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
 CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
 CC
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CC EMBL: M27638; AAA61337.1; -
 DR EMBL: X07880; CAA30727.1; -
 DR PIR: PLO102; AVM535.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19; 1.
 DR IMMUNOGLOBULIN V region; Signal.
 KW SIGNAL 1 18
 FT CHAIN 19 137
 FT DOMAIN 19 48 IG HEAVY CHAIN V REGION MOPC 315.
 FT DOMAIN 49 54 FRAMEWORK 1.
 FT DOMAIN 55 68 COMPLEMENTARTY-DETERMINING 1.
 FT DOMAIN 69 84 FRAMEWORK 2.
 FT DOMAIN 85 116 COMPLEMENTARTY-DETERMINING 2.
 FT DOMAIN 117 126 FRAMEWORK 3.
 FT DOMAIN 127 137 COMPLEMENTARTY-DETERMINING 3.
 FT DISULFID 40 114 BY SIMILARITY.
 FT CONFLICT 15 15 G -> GG (IN CAA30727).
 FT CONFLICT 15 15 G -> H (IN REF. 2).
 FT CONFLICT 77 78 GY -> YG (IN REF. 4).
 FT CONFLICT 102 102 N -> D (IN REF. 4).
 FT CONFLICT 123 123 MISSING (IN REF. 4).
 FT NON_TER 137 137
 FT SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match 54.5%; Score 408; DB 1; Length 137;
 Best Local Similarity 60.3%; Pred. No. 3.3e-32;
 Matches 85; Conservative 18; Mismatches 32; Indels 6; Gaps 4;

QY 1 MKHLNFFLLVAPRNVLSVQLOQWAGLTKRPSFLSLTCAVYGGSF--SGYWSMIRPP 59
 DB 1 MKVLSLYLLTALP-CIMSDVQLQESGPGLVKPSQSLTCAVYGGSF--SGYWSMIRPP 59
 QY 60 PGKGLMEIGELNHSSTNPSFLSLTCAVYGGSF--SGYWSMIRPP 119
 DB 60 PGKGLMEIGELNHSSTNPSFLSLTCAVYGGSF--SGYWSMIRPP 117
 QY 120 ARPH-RYFDYWGQGLTVTVSS 139
 DB 118 -NDHLYFDYWGQGLTVTVSS 137

RESULT 4

HV2G_HUMAN STANDARD; PRT; 117 AA.
 ID HV2G_HUMAN
 AC P01825;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE IG HEAVY CHAIN V-II REGION NEMM.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77242302; PubMed=407927;
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
 RT "Amino acid sequence of the VH region of a human myeloma
 immunoglobulin (IgG New).";
 RL Biochemistry 16:3412-3420(1977).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE=78066916; PubMed=618887;
 RA Saul F.A., Amzel L.M., Poljak R.J.;
 RT "Preliminary refinement and structural analysis of the Fab fragment
 from human immunoglobulin new at 2.0-A resolution.";
 RL J. Biol. Chem. 253:585-597(1978).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 PROTEIN.
 DR PIR: A02100; G1H0NM.
 DR PDB: 7FAB; 31-JAN-94.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19: 1.
 KW Immunoglobulin V region; 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT STRAND 3 7
 FT TURN 11 12
 FT STRAND 14 15
 FT TURN 18 25
 FT STRAND 30 31
 FT TURN 33 39
 FT STRAND 41 42
 FT TURN 46 51
 FT STRAND 53 54
 FT TURN 57 59
 FT STRAND 61 63
 FT HELIX 64 66
 FT TURN 67 72
 FT STRAND 73 76
 FT TURN 77 82
 FT STRAND 87 89
 FT HELIX 91 98
 FT STRAND 104 107
 FT STRAND 111 115
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match 53.1%; Score 397.5; DB 1; Length 117;
 Best Local Similarity 64.2%; Pred. No. 2.8e-31;
 Matches 77; Conservative 19; Mismatches 21; Indels 3; Gaps 1;

QY 20 OVLOQMGGLKPSFELSLTCAVYGGSGGYWMTROPFGGLEWIGINSGSTNYN 79
 DB 1 QVLEQSGPELVPSQSLTCTVSGSTFSDNYTWKOPGRLGIVFYHGHSDDT 60
 QY 80 PSIKSHVTISVDPSKQPSLKSSTVTAADPAVYVCAREIAPARHRYEDYGGQGLTVYSS 139
 DB 61 TPLRSVMTLVDSKQPSLKSSTVTAADPAVYVCARNLIA---GCCIDVWGQGSIVTVSS 117

RESULT 5
 HY60_MOUSE STANDARD; PRT; 116 AA.
 AC P18531:
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION M315 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 DR PIR: J0509; HVMS31.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19: 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 116
 FT DOMAIN 19 48 IG HEAVY CHAIN V REGION M315.
 FT DOMAIN 49 53 FRAMEWORK 1.
 FT DOMAIN 54 67 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 68 84 FRAMEWORK 2.
 FT DOMAIN 85 116 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 40 114 FRAMEWORK 3.
 FT NON_TER 116 116 BY SIMILARITY.
 SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 49.5%; Score 370; DB 1; Length 116;
 Best Local Similarity 64.1%; Pred. No. 1.1e-28;
 Matches 75; Conservative 15; Mismatches 25; Indels 2; Gaps 2;

QY 1 MKHLMEFLLVAPRWLSQVLOQMGGLKPSFELSLTCAVYGGSGF-SGYWMTROP 59
 DB 1 MKVSLTYLLTALP-GLISVOLQESGGLVKPSQSLTCTVSGSTVITGYSWVWNRKP 59
 QY 60 PGKLEWIGINSGSTNPNPSLKSRYTISVDTSKNOFSLKSVPADPAVYVCAR 116
 DB 60 PGKLEWIGIYSDGSSNNPNPSLKNRISITRDTSKNOFSLKINSVTTEDATFYCAR 116

RESULT 6
 HY43_MOUSE STANDARD; PRT; 144 AA.
 AC P01819:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION MOPC 141 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81012133; PubMed=6774258;
 RA Sakano H., Makl R., Kurosawa Y., Roeder W., Tonegawa S.;
 RT "Two types of somatic recombination are necessary for the generation
 of complete immunoglobulin heavy-chain genes.";
 RL Nature 286:676-683(1980).
 CC -I- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
 DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL: J00491; AAA38121.1; -
 CC EMBL: V00768; CAA24149.1; -
 CC PIR: A02094; G2MS14.
 CC INTERPRO: IPR003006; -
 CC PFAM: PF00047; 19: 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.


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DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
FT DOMAIN 19 48 FRAMEWORK 1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 54 67 FRAMEWORK 2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match
Best Local Similarity 45.9%; Score 343; DB 1; Length 116;
Matches 71; Conservative 16; Mismatches 28; Indels 2; Gaps 2;

QY 1 MKHLWFFLLVAAPRWLVSOVLOQMGAGLLKPSFTLSLTCVAYGSGF-SGYYSWMIROP 59
1 MRVLLILCLFTAPF-GILSDVQIQESGPDLYKPSQSLSLTCVTVGTGYSGYSMHWIRPF 59
Db 116

QY 60 PGKGLWIGGINSGSTNPNLSKRVTVISVDTSKNOFSLSSVTAADPAVYYCAR 116
116
Db 60 PGKLEMGVHYHSGNTSYNPSLSKRSISTRTSKNOFQLNLSVTEDEYATYYCAR 116
116

RESULT 10
HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6;
RX MEDLINE-81234548; PubMed-6788376;
RX Baltschell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00529; AAA38170.1; -
CC PIR; A02034; MHMS18.
CC INTERPRO; IPR003006; -
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT NON_TER 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.

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FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DDA4FDC9F465 CRC64;

Query Match
Best Local Similarity 44.1%; Score 330; DB 1; Length 139;
Matches 67; Conservative 22; Mismatches 42; Indels 2; Gaps 2;

QY 8 LLLVAAPRWLVSOVLOQMGAGLLKPSFTLSLTCVAYGSGFSGYYSWMIROPKGLWMI 67
8 LFLAATRTGVHSGVSOVLOQMGAGLLKPSFTLSLTCVAYGSGFSGYYSWMIROPKGLWMI 67
Db 68 GRDPNPGSGGKRYNKEKRSKATLVVDKPSRYAVQMSLSLSEDSAVYYCAR-YYYGSSVF 126
127 DYWGQGLTVYSS 139
Db 127 DYWGQGLTVYSS 139

RESULT 11
HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-81234548; PubMed-6788376;
RX Baltschell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00539; AAA38172.1; -
CC PIR; A02038; G2MS43.
CC INTERPRO; IPR003006; -
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BFA4B8BC9 CRC64;

Query Match
44.0%; Score 329; DB 1; Length 137;

```

Best Local Similarity 49.6%; Pred. No. 1.1e-24;
Matches 66; Conservative 22; Mismatches 41; Indels 4; Gaps 2;

OY 8 LILVAPRWLISQVLOQMGAGLLKPSFTSLTCAVYGGSGFSGYWMSWIRPPGKGLWEI 67
DB 8 LFLAAATGATGHSVOVLOQPGAEFTVKGPAVSLCKASGATFTSYLHMWVORGRGLEWI 67
OY 68 GEIN-HSGSTNPNPSLRVTISVDTSKNOFSLKLSVTADTAVYCARREIARPHRYF 126
DB 68 GRDPNPGSGTVEHFRSKATLTIDKPSSTAVYQGLSLISEDSAVYYCAR---YRLGRYF 124
OY 127 DYWGCGTLTVSS 139
DB 125 DYWGCGTLTVSS 137

RESULT 12
HV37_MOUSE STANDARD; PRT; 119 AA.

AC P01807;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION X44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudnikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
its potential role in generating diversity in
complementarity-determining regions."
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
THAT BINDS GALACTAN.
DR PIR: A02077; AVMSX4.
DR HSSP: P01810; 2F8J.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region.
FT NON_TER 119
SQ SEQUENCE 119 AA; 13246 MW; BC34FC8F31CDA1B3 CRC64;

Query Match 43.9%; Score 328; DB 1; Length 119;
Best Local Similarity 54.5%; Pred. No. 1.2e-24;
Matches 66; Conservative 17; Mismatches 34; Indels 4; Gaps 2;

OY 20 OVOLQMGAGLLKPSFTSLTCAVYGGSGFSGYWMSWIRPPGKGLWEIINHSST-NY 78
DB 1 EVKLLSGGGLVOPGGSLKLSCAASGDFSRVWMSWVROAPGKGLWEIINDSSSTIN 60
OY 79 NPSLKRVTISVDTSKNOFSLKLSVTADTAVYCARREIARPHRYFYWGCGTLTVSS 138
DB 61 TSLKXKFTISRMAKNTLTLYLQMSKYRSEDYALYCAR---LHYGYAAYWGCGTLTVSS 117
OY 139 S 139
DB 118 A 118

RESULT 13
HV62_MOUSE STANDARD; PRT; 117 AA.
AC P18533;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 733 PRECURSOR.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response."
J. Exp. Med. 169:2007-2019(1989).
DR PIR: J0510; HVMS73.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DISULFID 40 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 43.6%; Score 326.5; DB 1; Length 117;
Best Local Similarity 57.6%; Pred. No. 1.6e-24;
Matches 68; Conservative 15; Mismatches 32; Indels 3; Gaps 2;

OY 1 MKHLMFLLVAPRWVLSQVLOQMGAGLLKPSFTSLTCAVYGGSGFS--GYWMSWIR 58
DB 1 MKMFTLLYLTVVP-GILSDVQLQESGPGVLRKPSGIALTCYTGTSITGNRMWMI 59
OY 59 PGKGLWEIINHSSTNPNPSLRVTISVDTSKNOFSLKLSVTADTAVYCAR 116
DB 60 FPGNKLEWIGYIYSAITSYNSPSPKSRRTITRDTSKNOFLEMSILTAEADTAVYCAR 117

RESULT 14
HV38_MOUSE STANDARD; PRT; 119 AA.

AC P01808;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudnikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
its potential role in generating diversity in
complementarity-determining regions."
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
THAT BINDS GALACTAN.
DR PIR: A02078; AVMS76.
DR HSSP: P01810; 2F8J.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region.
FT NON_TER 119
SQ SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;

Query Match 43.6%; Score 326; DB 1; Length 119;
Best Local Similarity 54.5%; Pred. No. 1.8e-24;
Matches 66; Conservative 16; Mismatches 35; Indels 4; Gaps 2;

OY 20 OVOLQMGAGLLKPSFTSLTCAVYGGSGFSGYWMSWIRPPGKGLWEIINHSST-NY 78
DB 1 EVKLLSGGGLVOPGGSLKLSCAASGDFSRVWMSWVROAPGKGLWEIINDSSSTIN 60

QY 79 NPSLKSRTVISVDTSKNPSLKLSSVTAAADTAVYYCAREIARPHRYFDYWGQGLTVTS 138
 DB 61 TPSLKDCKFTISRDNMAKNSLYLQMSKVSSEDTALYYCAR--LGYGYFPWGWGGLTVTVS 117
 QY 139 S 139
 DB 118 S 118

RESULT 15

HY40.MOUSE
 ID HY40.MOUSE STANDARD: PRT: 119 AA.
 AC P01810;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION J539.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP PRELIMINARY SEQUENCE.
 RX MEDLINE-79223895; PubMed-111245;
 RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;
 RT "Structural evidence for independent joining region gene in
 RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
 RT its potential role in generating diversity in
 RT complementarity-determining regions."
 RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE-88217852; PubMed-3449853;
 RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
 RA Davies D.R.;
 RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
 RT study at 2.6-A resolution."
 RL Proteins 1:74-80(1986).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS GALACTAN.
 CC DR A02080; AVMSJ5.
 DR PDB: 2FBJ; 15-OCT-90.
 DR INTERPRO: IPR003006; -
 DR PFM: PF00047; 19; 1.
 KW Immunoglobulin V region; 3D-structure.
 FT NON_TER 119
 FT STRAND 3
 FT STRAND 10
 FT STRAND 12
 FT STRAND 14
 FT STRAND 15
 FT STRAND 18
 FT STRAND 25
 FT HELIX 29
 FT STRAND 31
 FT STRAND 34
 FT STRAND 39
 FT STRAND 41
 FT STRAND 42
 FT STRAND 45
 FT STRAND 51
 FT STRAND 53
 FT STRAND 54
 FT STRAND 58
 FT STRAND 60
 FT STRAND 62
 FT STRAND 67
 FT STRAND 72
 FT STRAND 78
 FT STRAND 83
 FT HELIX 88
 FT HELIX 90
 FT STRAND 92
 FT STRAND 100
 FT STRAND 101
 FT STRAND 103
 FT STRAND 104
 FT STRAND 108
 FT STRAND 112
 FT STRAND 116
 SQ SEQUENCE 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;

Query Match

Best Local Similarity 43.4%; Score 325; DB 1; Length 119;
 Matches 65; Conservative 19; Mismatches 33; Indels 4; Gaps 2;

QY 20 OYOLQMGAGLKPSTTSLTCAVYGSGFSGYWSIRPPGKGLFWIGELN-HSGSTNY 78
 DB 1 EYKLESGGGLVPGGSLKSLCAASGDFPSKYWMSVVRQAPGKGLWIGELIHPSDSTINY 60

QY 79 NPSLKSRTVISVDTSKNPSLKLSSVTAAADTAVYYCAREIARPHRYFDYWGQGLTVTS 138
 DB 61 TPSLKDCKFTISRDNMAKNSLYLQMSKVSSEDTALYYCAR--LHYGYNNYWGQGLTVTVS 117
 QY 139 S 139
 DB 118 A 118

Search completed: March 9, 2001, 16:46:04
 Job time: 178 sec

Fri Mar 9 16:49:08 2001

us-09-203-768a-2.rsp

Page 8

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: March 9, 2001, 16:43:41 ; Search time 38.3 seconds
(without alignments)
425.376 Million cell updates/sec

Title: US-09-203-768a-2
Perfect score: 748
Sequence: 1 MKHLMPFLLVAAERWVLSQ.....ARPHRPDYMGQGLTVTVSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:REMBL_15.*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	552	73.8	150	4	095973	095973 homo sapien
2	490.5	65.6	119	4	090L73	090L73 homo sapien
3	371	49.6	122	4	090L75	090L75 homo sapien
4	354.5	47.4	298	11	090YF0	090YF0 mus musculi
5	328.5	43.9	82	4	075725	075725 homo sapien
6	314	42.0	122	4	090L84	090L84 homo sapien
7	313.5	41.9	121	4	090L96	090L96 homo sapien
8	312.5	41.8	117	11	090XF0	090XF0 mus musculi
9	312	41.7	78	4	075739	075739 homo sapien
10	308.5	41.2	117	11	090XE9	090XE9 mus musculi
11	308.5	41.2	131	4	090L88	090L88 homo sapien
12	305.5	40.8	113	4	090L90	090L90 homo sapien
13	305	40.8	124	4	090L92	090L92 homo sapien
14	304.5	40.7	121	4	090L71	090L71 homo sapien
15	304	40.6	147	4	09Y509	09Y509 homo sapien
16	296.5	39.6	75	4	075743	075743 homo sapien
17	296.5	39.6	118	4	090L74	090L74 homo sapien
18	295	39.4	118	4	090L72	090L72 homo sapien
19	292.5	39.1	125	4	090L95	090L95 homo sapien

20	291	38.9	118	4	090L91	090L91 homo sapien
21	288.5	38.6	116	4	090L93	090L93 homo sapien
22	287	38.4	118	11	092L14	092L14 mus musculu
23	286	38.2	437	11	09R1A4	09R1A4 mus musculu
24	284.5	38.0	119	4	090L94	090L94 homo sapien
25	283	37.8	110	11	090L77	090L77 mus musculu
26	278.5	37.2	88	4	075737	075737 homo sapien
27	276	36.9	116	4	090L89	090L89 homo sapien
28	274	36.6	109	11	090L75	090L75 mus musculu
29	269.5	36.0	117	11	092L16	092L16 mus musculu
30	266.5	35.6	109	11	090L85	090L85 mus musculu
31	266	35.6	124	6	090N06	090N06 oryctolagus
32	265	35.4	114	11	090L81	090L81 mus musculu
33	264.5	35.3	150	4	09Y298	09Y298 homo sapien
34	264	35.3	124	6	090N04	090N04 oryctolagus
35	259.5	34.7	112	4	090GP3	090GP3 homo sapien
36	256.5	34.3	95	4	090LB6	090LB6 homo sapien
37	256.5	34.3	157	4	095978	095978 homo sapien
38	255.5	34.2	104	4	090L87	090L87 homo sapien
39	245	32.8	97	4	043234	043234 homo sapien
40	238	31.8	110	11	090L83	090L83 mus musculu
41	224.5	30.0	77	4	075741	075741 homo sapien
42	223.5	29.9	102	11	090L79	090L79 mus musculu
43	218	29.1	416	4	09NP6	09NP6 homo sapien
44	216.5	28.9	78	4	075730	075730 homo sapien
45	208	27.8	80	4	075727	075727 homo sapien

ALIGNMENTS

RESULT 1
ID 095973 PRELIMINARY: PRT: 150 AA.
AC 095973;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE V44 HEAVY CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of Igm secreting B cell in the synovium of
RT Behcet's patient with arthritis.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -
DR HSSP; P01825; 7FAB.
DR INTERPRO: IPR003006; -
DR PFAM; PF00047; 19; 1.
KW Signal.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 >150 V44 HEAVY CHAIN VARIABLE REGION.
FT NON TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938A7C9 CRC64;

Query Match 73.8%; Score 552; DB 4; Length 150;
Best local Similarity 76.8%; Pred. No. 5.8e-49;
Matches 109; Conservative 11; Mismatches 14; Indels 8; Gaps 3;

QY 1 MKHLMPFLLVAAERWVLSQVLOQNGAGLTKPSEFLSLTCAYVGGSF--GYGSMIRQ 58
DB 1 MKHLMPFLLVAAERWVLSQVLOQNGAGLTKPSEFLSLTCAYVGGSF--GYGSMIRQ 60
QY PPKGGEIWEIGINHSSTNVPISLKSRTVTSVDTSKNPSLKSSTVADTAVYCAR-E 117
DB 61 PPKGGEIWEIGINHSSTNVPISLKSRTVTSVDTSKNPSLKSSTVADTAVYCARLG 120

Qy	118	IAARPHRYFDYWGQGLTVVSS	139
		: :	
Db	121	MGA-----FDFWGHGIMTVVSS	137

RESULT	2		
09UL73			
ID	Q9UL73	PRELIMINARY;	PTT; 119 AA.
AC	Q9UL73;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)		
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)		
OS	Homo sapiens (Human) .		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,		
RA	Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal		
RT	fetus.";		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL: AF035041; AAD56277.1; -.		
DR	INTERPRO: IPR003006; -.		
DR	PRAM: PF00047; 1g; 1.		
FT	NON_TER 1		
FT	NON_TER 119 119		
SO	SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EAOBE CRC64;		

SEQUENCE	122 AA:	13719 MR:	56CB0612586A5529 CRC64:
SO	SEQUENCE	122 AA:	13719 MR: 56CB0612586A5529 CRC64:
FT	NON_TER	1	1
DR	PFAM: PF00047:	19: 1.	
DR	INTERPRO: IPR003006:	-	
DR	EMBL: AF035039:	AAD56275.1:	-
RL	Clin. Immunol. Immunopathol.	87:184-192(1998).	
RL	EMBL: AF035039:	AAD56275.1:	-
RT	Young D C.:		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".		
RA	Young D C.:		
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,		
RA	Medline=98277139:	Pubmed=9614934:	
RN	SEQUENCE FROM N.A.		
OX	NCBI_TaxId=9606;		
OC	Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.		
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;		
OS	Homo sapiens (Human).		
OS	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)		
DT	01-JUN-2000 (TREMBLrel. 14, last annotation update)		
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)		
ID	09UL75:		
ID	PRELIMINARY:	PRT: 122 AA.	
RESULT	3		

Query Match Similarity	49.6%	Score 371;	DB 4;	Length 122;
Best Local Similarity	61.3%	Pred No.1,4e-30;		
Matches	76;	Conservative 15;	Mismatches 27;	Indels 6;
				Gaps 3
QY	20	QVQLQQMGAGLKPSETLSLTCAVYGGSPS--GYWSWIRQPPGKGLWIGELINHSGS--	75	
		: : : : : : : :		
DB	1	QVQLQSGGGLVLPQSTLSLTCAISGDSVSNSAAMNWTQSPRGLWLGRTYYSKMY	60	
QY	76	TINYNSLKSRLVTISVDTSKNPSFLKLSSTAAIDVAVYYCARETIAARPHRYFDYWGQGLV	135	
		: : : : : : : : : : : : : : : : : : : : : :		
DB	61	NDYRVSYSKSRITINPDTSKNPSFLQNSVTPEDTAVYYCARDELGLGQ--FDYWGQGLV	118	
QY	136	TVSS	139	
DB	119	TVSS	122	

Q90YF0	4	RESULT
ID	Q90YF0	PRELIMINARY; PRT; 298 AA.
AC	Q90YF0;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TrEMBLrel. 15, last annotation update)	
DE	CN 8 SCFV.	
GN	CN 8.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	SPRAIN-BALB/C; TISSUE=SPLEEN;	
RA	Shinozawa N., Demura T., Fukuda H.;	
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	SPRAIN-BALB/C; TISSUE=SPLEEN;	
RA	Shinozawa N., Demura T., Fukuda H.;	
RL	"Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtraction method."	
RT	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AB036341; BA88633.1; -	
DR	HSSP: P01607; 1REI.	
DR	INTERPRO: IPR003006; -	
DR	PFAM: PF00047; 1g; 2.	
Q9	SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;	

RESULT	5	
075725		
ID	075725	PRELIMINARY;
AC	075725;	PRT;
DT	01-NOV-1998 (TREMblrel, 08, Created)	82 AA

DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, last annotation update)
GN IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RA Fischer M., Kuepers R.,
"Human Iga and IgM secreting intestinal plasma cells carry heavily
mutated VH region genes.";
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ009522; CA08729.1;
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
DR INTERPRO: IPR003006;
PF PFAM: PF00047; 1g; 1.
FT NON_TER 1
FT 82
SQ SEQUENCE 82 AA; 9566 MW; 4325325C6570987A CRC64;

Query Match 43.9%; Score 328.5; DB 4; Length 82;
Best Local Similarity 74.4%; Pred. No. 1.9e-26;
Matches 61; Conservative 7; Mismatches 13; Indels 1; Gaps 1;
QY 49 SGYWSWIRPGKGLGELINHSSTPNYNSLKSRTVISDTSKNOFSLKSSVTAD 108
DB 1 SNEYMGWIRPGKGLGELINHSSTPNYNSLKSRTVISDTSKNOFSLKSSVTAD 60
QY 109 TAVYYCAREI-AARPHRYFDYW 129
DB 61 TAVYYCARFEGGRAMPYFDYW 82

RESULT 6
Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035030; AAD56266.1;
DR HSSP: P01772; 2P84
DR INTERPRO: IPR003006;
DR PFAM: PF00047; 1g; 1.
FT NON_TER 1
FT 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 42.0%; Score 314; DB 4; Length 122;
Best Local Similarity 51.6%; Pred. No. 9.3e-25;
Matches 63; Conservative 19; Mismatches 38; Indels 2; Gaps 2;
QY 20 OVLODMGAGLKPESTSLTCAYVGGSGYWMIRPGKGLGELINHSSTN-Y 78
DB 1 EVOLVESGGGVQPSRLKSCASASRTFSNYGMHWIAROPGKGLGELVAAISNDGSKFY 60

QY 79 NPSLKSRTVISDTSKNOFSLKSSVTADTAVYYCARIAR-PHRYFDYWGQTLTV 137
DB 61 ADVSVGRFTIPDNKSNMMDLQMSLRADTAVYYCANDERGLVGYFDYWGQTLTV 120
QY 138 SS 139
DB 121 SS 122

RESULT 7
Q9UL96 PRELIMINARY; PRT; 121 AA.
AC Q9UL96;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035018; AAD56254.1;
DR INTERPRO: IPR003006;
DR PFAM: PF00047; 1g; 1.
FT NON_TER 1
FT 121
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BD35 CRC64;

Query Match 41.9%; Score 313.5; DB 4; Length 121;
Best Local Similarity 52.3%; Pred. No. 1e-24;
Matches 67; Conservative 14; Mismatches 32; Indels 15; Gaps 3;
QY 20 OVLODMGAGLKPESTSLTCAYVGGSF--SGYWSWIRPGKGLGELINHSSTN 77
DB 1 QITLKESGFTLVKPTQTLVLTCTGFSGLTSGMVGVGIRPGKGLALVYDDDKR 60
QY 78 VNPSSLKSRVTISVDTSKNOFSLKSSVTADTAVYYCAREIARHR-----YFDYWGQ 131
DB 61 YSPSLKSRVTITKDYTSKNQVDLTMFMDFMDPATYYCA-----HRSKGQGYFDYWGQ 113
QY 132 GLTVTVSS 139
DB 114 GLTVTVSS 121

RESULT 8
Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ225171; CAB65236.1;
DR INTERPRO: IPR003006;
DR PFAM: PF00047; 1g; 1.

FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 13060 MW: D816AD0858A47EAC CRC64;

Query Match
Best Local Similarity 41.8%; Score 312.5; DB 11; Length 117;
Matches 58; Conservative 26; Mismatches 32; Indels 5; Gaps 2;

OY 20 QVQLDQWAGLLKPSSETLSLTCAVYGGSGFYWSMIRPPKGLGEMIGELIN-HSGSTNY 78
Db 1 EVQLDQSGELVKGPGASVMSCKASGYTFDYMMKWKSHGKSLKLEIGDIPNNNGTSTY 60
OY 79 NPSLKSRTVTSVDTSKNPSLKLSSVTAADTAAYVYCAREIARPHRYF-DYWGCGTLVTF 138
Db 61 NQKFKGKATLVKDKSSSTAYMQLNSLTSEDSAVYYCARD----KDYFFYMGCGTTLVTS 116
OY 139 S 139
Db 117 S 117

RESULT 9
OY 075739 PRELIMINARY; PRT; 78 AA.
AC 075739;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RA Flicher M., Kuipers R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ009538; CAA08743.1; -
DR INTERPRO: IPR003006; -
DR PFM: PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA: 9031 MW: 2EB52A6C7A488066 CRC64;

Query Match
Best Local Similarity 41.7%; Score 312; DB 4; Length 78;
Matches 58; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 52 YMSWIRPPGKLEWIGELINHSSTNYNPSLKSRTVTSVDTSKNPSLKLSSVTAADTAAY 111
Db 1 YMSWIRPPGKLEWIGELINHSSTNYNPSLKSRTVTSVDTSKNPSLKLSSVTAADTAAY 60
OY 112 YVCARHSSSWPIYFDNW 129
Db 61 YVCARHSSSWPIYFDNW 78

RESULT 10
OY 090X9 PRELIMINARY; PRT; 117 AA.
AC 090X9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ225174; CAB65237.1; -
DR INTERPRO: IPR003006; -
DR PFM: PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 13000 MW: CDE2AF84D499734 CRC64;

Query Match
Best Local Similarity 41.2%; Score 308.5; DB 11; Length 117;
Matches 59; Conservative 26; Mismatches 23; Indels 9; Gaps 3;

OY 20 QVQLDQWAGLLKPSSETLSLTCAVYGGSGFYWSMIRPPKGLGEMIGELIN-HSGSTNY 78
Db 1 EVQLDQSGELVKGPGASVMSCKASGYTFDYMMKWKSHGKSLKLEIGDIPNNNGTSTY 60
OY 79 NPSLKSRTVTSVDTSKNPSLKLSSVTAADTAAYVYCAREIARPHRYF-DYWGCGTLVTF 136
Db 61 NQKFKGKATLVKDKSSSTAYMQLNSLTSEDSAVYYCARD-----RYAMDYMGCGTSTV 114
OY 137 VSS 139
Db 115 VSS 117

RESULT 11
OY 090L88 PRELIMINARY; PRT; 131 AA.
AC 090L88;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetuses".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035026; AAD56262.1; -
DR INTERPRO: IPR003006; -
DR PFM: PF00047; 1g; 1.
FT NON_TER 1 1
FT NON_TER 131 131
SQ SEQUENCE 131 AA: 14142 MW: 96E7D668E375DEA0 CRC64;

Query Match
Best Local Similarity 41.2%; Score 308.5; DB 4; Length 131;
Matches 63; Conservative 20; Mismatches 37; Indels 11; Gaps 2;

OY 20 QVQLDQWAGLLKPSSETLSLTCAVYGGSGFYWSMIRPPKGLGEMIGELIN-HSGSTNY 76
Db 1 EVQLDQSGELVKGPGASVMSCKASGYTFDYMMKWKSHGKSLKLEIGDIPNNNGTSTY 60
OY 77 NPSLKSRTVTSVDTSKNPSLKLSSVTAADTAAYVYCAREIARPHRYF-DYWGCGTLVTF 128
Db 61 DVAAPVKGRLTISRSSKNTLVLRNLSKTEDTAVYCTGTITLIVITTSKRTSEY 120
OY 129 WGCGTLVYSS 139
Db 117 WGCGTLVYSS 139

DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers."
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; A014339.1; -
DR HSSP: P01772; 2F84
DR INTERPRO: IPR003006; -
DR PFM; PF00047; 19; 1.
FT NON_TER 1
SQ SEQUENCE 147 AA; 15768 MW; 8489FCNAA7BC925C CRC64;

Query Match 40.6%; Score 304; DB 4; Length 147;
Best Local Similarity 48.1%; Pred. No. 1.2e-23;
Matches 63; Conservative 20; Mismatches 32; Indels 16; Gaps 3;
QY 20 OYOLQOMGAGLKPSELTSLTCAVYGGSGYYSWIRQPGKLEWIGEINHSSTNYN 79
DB 1 QYHVESGGGVOPGKSLRSCASGFTSTYGMWVROAPGKGLDWALISTDGSSTQY 60
QY 80 P-SLKSRTISVDTSKNQFSLKLSVTAADTAVYYCAREIAARPHRYF-----DY 128
DB 61 ACSVKGRTISRDNKNTLYLQWTSLRVEDTAVYYCAKD-----GNYPDSVGYVAGIDY 115
QY 129 WGQGTLYTVSS 139
DB 116 WGQGTLYTVSS 126

Search completed: March 9, 2001, 16:46:47
Job time: 186 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2001, 16:43:34 ; Search time 26.57 Seconds
(without alignments)
150.571 Million cell updates/sec

Title: US-09-203-768a-4
Perfect score: 615
Sequence: 1 LMPLPTGGEIVMTQSPATLS.....QYNNMPYTFGGQTKLEIKR 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseqp/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseqp/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseqp/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseqp/AA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseqp/AA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseqp/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseqp/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseqp/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseqp/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseqp/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseqp/AA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseqp/AA1995.DAT:*
- 17: /SIDSL/gcgdata/geneseq/geneseqp/AA1996.DAT:*
- 18: /SIDSL/gcgdata/geneseq/geneseqp/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538.5	87.6	234	15	R52951 Human anti-IgE Mab
2	528.5	85.9	213	20	Y14207 HIV-1 gp120 peptid
3	528.5	85.9	213	20	Y14211 HIV gp120 protein
4	525	85.4	128	21	Y56720 Amino acid sequenc
5	523	85.0	129	14	R38672 VK325-Jk2. Homo s
6	518	84.2	117	19	W47582 Human monoclonal a
7	513.5	83.5	349	12	R12128 IBI IgG aberrant 1
8	513.5	83.5	414	12	R13111 IBI IgG aberrant 1
9	513.5	83.5	414	12	R13018 IBI IgG aberrant 1
10	510.5	83.0	234	21	Y92239 Human bone marrow-
11	509.5	82.8	214	20	Y06842 Seq ID No:10 of JP
12	504.5	82.0	134	17	W11155 Anti-lung tumour a

13	499	81.1	129	14	R41286 F105 rearranged va
14	497	80.8	129	14	R38673 F105JK. Ho
15	494	80.3	150	19	W40069 Human monoclonal a
16	493.5	80.2	401	12	R12129 ORF 1 of IgG light
17	490.5	79.8	127	20	W08946 kappa light chain
18	489	79.5	109	20	Y08230 Human ScFv light c
19	489	79.5	115	14	R38648 Human V-kappa frag
20	489	79.5	115	15	R62928 Human V-kappa vk65
21	489	79.5	115	18	W41144 Human vkappa65.3 f
22	489	79.5	115	19	W62182 Human DNA vkappa65
23	482.5	78.5	214	20	Y08599 Anti-human TNF- α p
24	480	78.0	124	18	W24539 Immunoglobulin F10
25	476.5	77.5	120	17	W03946 DNA fragment vk65.
26	475.5	77.3	127	15	R50192 Light chain variab
27	475.5	77.3	127	20	Y26982 Light chain variab
28	474.5	77.2	109	20	W84096 Human V kappa subg
29	474	77.1	110	18	W27545 Human Ab light cha
30	474	77.1	115	20	Y40429 Anti-P. aeruginosa
31	469.5	76.3	127	15	R50187 Light chain variab
32	469.5	76.3	127	20	Y26980 Light chain variab
33	469.5	76.3	127	21	Y32407 Mouse anti-veitox
34	469.5	76.3	128	10	P91001 Anti-P. aeruginosa
35	466.5	75.9	127	15	R50191 Light chain variab
36	466.5	75.9	127	20	Y26981 Light chain variab
37	465	75.6	115	14	R38649 Human V-kappa frag
38	465	75.6	115	15	R62929 Human V-kappa vk65
39	465	75.6	115	17	W03947 DNA fragment vk65.
40	465	75.6	115	18	W41145 Human vkappa65.5 f
41	465	75.6	115	19	W62183 Human DNA vkappa65
42	465	75.6	115	20	Y40430 Amino acid sequenc
43	463.5	75.4	116	14	R38650 Human V-kappa frag
44	463.5	75.4	116	15	R62930 Human V-kappa vk65
45	463.5	75.4	116	17	W03948 DNA fragment vk65.

ALIGNMENTS

RESULT 1	
RS2951	234 AA.
ID	R52951 standard; Protein; 234 AA.
XX	
AC	R52951;
XX	
DT	27-OCT-1994 (first entry)
XX	
DE	Human anti-IgE Mab light chain.
XX	
KW	Human IgE; CH4 region; triggers mediator release;
KW	Mast cells; Monoclonal antibody; allergy.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	21..128
XX	/label= light chain variable region
XX	
PD	EP592230-A.
XX	
PD	13-APR-1994.
XX	
PF	07-OCT-1993; 93EP-0308006.
XX	
PR	07-OCT-1992; 92JP-0293800.
XX	
PA	(SNOW) SNOW BRAND MILK PROD CO LTD.
XX	
PI	Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;
PI	Yoshida T;
XX	
DR	WPI; 1994-120330/15.
XX	
DR	N-PSDB; Q71872.
XX	

PT Human monoclonal anti-19E peptide antibody - inhibits histamine
PT release from mast cells by allergen stimulation, useful for
PT preventing allergies
XX
XX Claim 3; Page 12; 21pp; English.
PS
XX R52951 shows the light chain of a human type anti-19E peptide
CC monoclonal antibody which inhibits the signal transmission for
CC the release of chemical mediator from mast cells and basophils
CC stimulated with allergen. The antibody can be used for the
CC prophylaxis and the therapy of allergy.
CC
XX Sequence 234 AA:
SQ

Query Match 87.6%; Score 538.5; DB 15; Length 234;
Best Local Similarity 87.9%; Pred. No. 1.6e-32;
Matches 102; Conservative 9; Mismatches 4; Indels 1; Gaps 1;

QY 1 LMLPTGTGIVMTOSPATLVSFGERATLSCRASOSVSSNLAWYOOKPGQAPRLILYGAS 60
DB 13 Lwlpdtgeiwmqspatlsvsbgpgraaalscrasqsvsnlamiyqkpkpqpaprlillygas 72
QY 61 TRATGIPARFSGSGTEFTLTITSSLOSEDFAVYYCOQYNNMPPTFGGQTKLEIK 116
DB 73 tratiqparfsgsgstftltitsslqsedfalycqyqysw-prtfgqtkvdlk 127

RESULT 2
Y14207
ID Y14207 standard; peptide: 213 AA.
XX
AC Y14207;
XX
DT 28-JUL-1999 (first entry)
XX
DE HIV-1 gp120 peptide.
XX
DE HIV, gp120; inhibitor; glycoprotein; CD4; leukocyte; infection.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO9924065-A1.
XX
PD 20-MAY-1999.
XX
PE 10-NOV-1998; 98WO-US23905.
XX
PR 18-JUN-1998; 98US-0100764.
PR 10-NOV-1997; 97US-0967708.
XX
PA (DAND) DANA FARBER CANCER INST INC.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Hendrickson WA, Kwong PD, Samanen JM, Sodroski JG;
PI Wyatt RT;
XX
DR WPI: 1999-337640/28.
XX
PT Inhibiting interaction between human immune deficiency virus gp120
PT and CD4
XX
PS Disclosure: Fig 20; 41pp; English.
XX
CC This sequence represents a region of the HIV-1 gp120 protein.
CC The invention relates to a method of inhibiting the interaction between
CC human immune deficiency virus (HIV) glycoprotein gp120 and CD4 on
CC leukocytes by administering an agent (I) containing functional groups
CC that interact with gp120 to disrupt at least two specified interactions.
CC (I) are used to treat and prevent infection by HIV.
XX
SQ Sequence 213 AA;

Query Match 85.9%; Score 528.5; DB 20; Length 213;
Best Local Similarity 91.8%; Pred. No. 7.8e-32;
Matches 101; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 9 EIVMTOSPATLVSFGERATLSCRASOSVSSNLAWYOOKPGQAPRLILYGASTRATGIPA 68
DB 1 eltlqspatlsvsfgeratlsctrasasesvslayqkpkpqpaprlillygastratgypa 60
QY 69 RFSGSGSGTEFTLTITSSLOSEDFAVYYCOQYNNMPPTFGGQTKLEIK 117
DB 61 rfsgsgsgteftltitsslqsedfavycqynmpptyrfggqtkleikr 110

RESULT 3
Y14211
ID Y14211 standard; peptide: 213 AA.
XX
AC Y14211;
XX
DT 28-JUL-1999 (first entry)
XX
DE HIV gp120 protein fragment.
XX
DE HIV, gp120; glycoprotein; X-ray diffraction crystal; drug design;
XX infection; therapy.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO9924553-A2.
XX
PD 20-MAY-1999.
XX
PE 10-NOV-1998; 98WO-US23905.
XX
PR 18-JUN-1998; 98US-0100763.
PR 10-NOV-1997; 97US-0966932.
PR 10-NOV-1997; 97US-0966987.
PR 10-NOV-1997; 97US-0967148.
PR 10-NOV-1997; 97US-0967403.
PR 24-NOV-1997; 97US-0976741.
PR 18-JUN-1998; 98US-0100521.
PR 18-JUN-1998; 98US-0100529.
PR 18-JUN-1998; 98US-0100631.
PR 18-JUN-1998; 98US-0100762.
XX
PA (DAND) DANA FARBER CANCER INST INC.
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Hendrickson WA, Kwong PD, Sodroski JG, Wyatt RT;
PI WPI: 1999-337709/28.
XX
DR Crystals of human immune deficiency virus gp120 glycoprotein
DR
XX
PT Crystals of human immune deficiency virus gp120 glycoprotein
PT
XX
PS Disclosure: Fig 53; 41pp; English.
XX
CC This sequence represents a HIV gp120 glycoprotein fragment.
CC The invention relates to crystals (A) for X-ray diffraction analysis
CC comprise a polypeptide (I) representing part of the human immune
CC deficiency virus (HIV) glycoprotein gp120. (A) are used to generate
CC atomic coordinates for rational drug design, i.e. identification or
CC design of agents that bind gp120, potentially useful for treating or
CC preventing HIV infection. Variants of gp120 having a hidden, conserved
CC neutralising epitope are useful in vaccines and to generate anti-HIV
CC antibodies.
XX
SQ Sequence 213 AA;

Query Match 85.9%; Score 528.5; DB 20; Length 213;
Best Local Similarity 91.8%; Pred. No. 7.8e-32;

Query Match 85.0%; Score 523; DB 14; Length 129;
 Best Local Similarity 87.3%; Pred. No. 1.2e-31;
 Matches 103; Conservative 7; Mismatches 6; Indels 2; Gaps 2;

OY 1 LMLPDTGEIWMQSPALVSFGERATLSCRASQSVSSN-IAMVQOKPGQAPRLIYGA 59
 |||
 DB 13 lwlptltgvtlspgtlslspgeratlscrasgsvssylawyqkpgqaprllyga 72
 OY 60 SRRATGIPARFSGSGSTFEFTLTISLQSEDFAVYCCQYNNMPPTFGQTKLEIKR 117
 |||
 DB 73 ssratgipdrfsgsgstfdltlrlslrlepedfayvcqyggs-spyltfgqtklelkr 129

RESULT 6
 W47582
 ID W47582 standard; Protein: 117 AA.
 AC W47582;
 DE 22-JUN-1998 (first entry)

XX Human monoclonal antibody light chain variable region.
 DE Human monoclonal antibody; hybridoma cell strain TTG6; hMab;
 KW antitetanus toxin.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH 24..34
 FT Region /Label= CDR1
 FT 49..55
 FT Region /Label= CDR2
 FT 89..98
 FT Region /Label= CDR3

PN JPI0014570-A.
 PD 20-JAN-1998.
 XX 05-JUL-1996; 96JP-0194095.
 PF 05-JUL-1996; 96JP-0194095.
 PR 05-JUL-1996; 96JP-0194095.
 XX (MATSU) MATSUDA M.
 PA (MONT) MORINAGA & CO LTD.
 DR MPI: 1998-138233/13.
 DR N-PSDB; V18674.

XX New cDNA encoding human monoclonal antibody - useful for production
 PT of antibody by hybridoma techniques commercially

PS Claim 4; Fig 2; 8pp; Japanese.

XX The present sequence represents a human monoclonal antibody (hMab)
 CC light chain variable region. The cDNA encoding the hMab can be used
 CC for commercial production of the hMab. The cDNA was isolated from an
 CC antitetanus toxin human monoclonal antibody producing hybridoma cell
 CC strain TTG6.

XX Sequence 117 AA;

Query Match 84.2%; Score 518; DB 19; Length 117;
 Best Local Similarity 90.8%; Pred. No. 2.6e-31;
 Matches 99; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 9 EIVMTQSPATLVSFGERATLSCRASQSVSSN-IAMVQOKPGQAPRLIYGA 68
 |||
 DB 1 divmtqspatlvsvfgeratlscrasgsvgtlnlawyqkpgqaprllygastratylaa 60

OY 69 RFGSGSGTFTLTISLQSEDFAVYCCQYNNMPPTFGQTKLEIKR 117
 |||
 DB 61 rtsgsgstfelftlslslqsedfayvcqygswppqtlfggtkveirr 109

RESULT 7
 R12128
 ID R12128 standard; Protein: 349 AA.
 XX R12128;

XX 01-AUG-1991 (first entry)

XX 1B1 IgG aberrant light chain with duplicated variable region.
 DE immunoglobulin G; light chain; variable region; duplication;
 KW passive immunity; group B streptococci.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH 1..17
 FT Peptide /Label= leader peptide
 FT 18..130
 FT Region /Label= variable region
 FT /note= "L'V 1"
 FT 131..243
 FT Region /Label= variable region
 FT /note= "L'V 2"
 FT 244..345
 FT Region /Label= constant region

PN W09106305-A.
 PD 16-MAY-1991.
 XX 06-NOV-1990; 90MO-US06426.
 PF 06-NOV-1990; 90MO-US06426.
 PR 07-NOV-1989; 89US-0432700.
 XX (BRIM) BRISTOL-MYERS SQUIB.

PA Shuford WW, Harris LJ, Raft HV;
 DR MPI: 1991-163947/22.
 DR N-PSDB; Q11878.

XX Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class

PS Example 5; Fig 16; 104pp; English.

XX This sequence is deduced from the cDNA clone 4B9-VK15 and includes
 CC the amino acid sequence beyond the first stop codon. The clone is
 CC incomplete, starting from the G of the ATG initiator codon, but the
 CC initial Met is given. Antibody molecules of the invention can
 CC include one or two aberrant light chains containing a duplicated
 CC variable region, to produce heavier antibodies. These heavier
 CC antibodies were found to have higher avidity than antibodies with
 CC just a single copy of the L'V region. The antibodies can be used to
 CC treat disease, e.g. infection by Streptococcus agalactiae. They are
 CC able to pass across the placenta.
 CC See also Q11879 and Q11880.

XX Sequence 349 AA;

Query Match 83.5%; Score 513.5; DB 12; Length 349;
 Best Local Similarity 85.5%; Pred. No. 1.5e-30;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY	1	LMEDPTGELTVMQSPATISVSPGRATISCPASQSVSNLAWYQOKPGQAPRLILIGAS	60
Db	13	lwpdttgelvllqspatllspgatalstcrasqsvsylvawqgdkp9qaprlilydas	72
QY	61	TRATGIPARPSGSGSEFTTLTISLSQEDPAVAYVYCOQYNNMP - YTFGGGTLEIK	116
Db	73	nratgipartsgsgstfcltlisslepedfayvycqhrdnwppgatffggktvkl	129
RESULT	8		
ID	R1311		
XX	AC	R1311 standard; Protein; 414 AA.	
XX	XX		
XX	R1311;		
DT	01-AUG-1991	(first entry)	
XX	XX		
DE	1b1	IgG aberrant light chain with duplicated variable region.	
XX	XX		
KM	immunoglobulin G; light chain; variable region; duplication;		
KW	passive immunity; group B streptococci.		
XX	XX		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..17	
FT		/label= leader peptide	
FT	Region	18..130	
FT		/label= variable region	
FT	Region	/note= "L/V 1"	
FT		131..243	
FT	Region	/label= variable region	
FT		/note= "L/V 2"	
FT	Region	244..345	
FT		/label= constant region	
XX	XX		
PN	W09106305-A.		
XX	XX		
PD	16-MAY-1991.		
XX	XX		
PE	06-NOV-1990;	90MO-US06426.	
XX	XX		
PR	07-NOV-1989;	89US-0432700.	
XX	XX		
PA	(BRIM)	BRISTOL-MYERS SQUIB.	
XX	XX		
PI	Shuford WM, Harris LJ, Raff HV;		
XX	XX		
DR	WPI; 1991-163947/22.		
DR	N-PSDB; Q11878.		
XX	XX		
PT	Oligomeric immunoglobulin(s) with high avidity for antigen(s) -		
PT	formed by duplicating esp. variable region of light chain of IgG		
PT	class		
XX	XX		
PS	Example 5; Fig 16; 104pp; English.		
XX	XX		
CC	CC	This sequence is deduced from the cDNA clone 4B9-VK15 and includes	
CC	CC	the amino acid sequence beyond the first stop codon ("X" in the	
CC	CC	sequence represents a nonsense codon). The clone is incomplete,	
CC	CC	starting from the G of the ATG initiator codon, but the initial Met	
CC	CC	is given. Antibody molecules of the invention can include one or two	
CC	CC	aberrant light chains containing a duplicated variable region, to	
CC	CC	produce heavier antibodies. These heavier antibodies were found to	
CC	CC	have higher avidity than antibodies with just a single copy of the	
CC	CC	L/V region. The antibodies can be used to treat disease, e.g.	
CC	CC	infection by Streptococcus agalactiae. They are able to pass across	
CC	CC	the placenta.	
CC	CC	See also Q11879 and Q11880.	
XX	XX		
XX	XX		
Sequence	414 AA;		

```

Query Match                               83.5%; Score 51.5; DB 12; Length 414;
Best Local Similarity                     85.5%; Pred.No. 1.8e-30;
Matches 100; Conservative      6; Mismatches 10; Indels    1; Gaps    1;

Oy   1 LMLPTTGEIWTQSPALVSPGCRATLSCRASQSVSSNLAWYQQKPKGPAPRLTIYGAS 60
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   13 LWpldtgeivltgtpalstspgeratlscraasqsvsyLawygdkpgqpdrprllydas 72
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy   61 TRANGIPARFSGSGSGETFEFTLTISLSQSEDFAVYYCQGYNNMPP-YTFGGGTKEIK 116
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   73 nratgiptarfsgsggdftltislsepedfavyycqhndmwpqatfggtkveik 129
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT          9
R13018 ID       R13018 standard; Protein; 414 AA.
XX AC         R13018;
DT           01-AUG-1991 (first entry) ;
XX DE        IB1 Igs aberrant light chain with duplicated variable region.
XX KW        Immunoglobulin G; light chain; variable region; duplication;
KM passive immunity; group B streptococci.
XX OS        Homo sapiens.
XX FH Key     Location/Qualifiers
FH FT Peptide 1..17
               /label= leader peptide
FT FT Region  18..130
               /label= variable region
               /note= "L/V 1"
FT FT Region  131..243
               /label= variable region
               /note= "L/V 2"
FT FT Region  244..345
               /label= constant region

XX PN WO9106305-A.
XX PD 16-MAY-1991.
XX PF 06-NOV-1990; 90WO-US06426.
XX PR 07-NOV-1989; 89US-0432700.
XX PA (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WM, Harris LJ, Raff HV;
XX WP: 1991-163947/22.
DR N-PSTDB; Q11878.

XX Oligomeric immunoglobulin(s) with high avidity for antigen(s). -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
Example 5; Fig 16; 104pp; English.

CC This sequence is deduced from the cDNA clone 4B9-VK15 and includes
CC the amino acid sequence beyond the first stop codon ("x" in the
CC sequence represents a nonsense codon). The clone is incomplete,
CC starting from the G of the ATG initiator codon, but the initial Met
CC is given. Antibody molecules of the invention can include one or two
CC aberrant light chains containing a duplicated variable region, to
CC produce heavier antibodies. These heavier antibodies were found to
CC have higher avidity than antibodies with just a single copy of the
CC L/V region. The antibodies can be used to treat disease, e.g.
CC infection by Streptococcus agalactiae. They are able to pass across
CC the placenta.
CC See also Q11879 and Q11880.
```

XX Sequence 414 AA:
SQ

Query Match 83.5%; Score 513.5; DB 12; Length 414;
Best Local Similarity 85.5%; Pred. No. 1.8e-30;
Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LWPDPITGEIVMTOSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGCAPRLIYGAS 60
DB 13 LWPDPITGEIVMTOSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGCAPRLIYGAS 72
OY 61 TRATGIPARFSGSGSTEFTLTSSLSQSDPAVYCYQOYNNMPP-YTFGGCKLEIK 116
DB 73 nratgiparfsgsgstgdflltsslepedfayycqhdnwpdgatfgggtkveik 129

RESULT 10
Y92239
ID Y92239 standard; Protein: 234 AA.

AC Y92239;
XX
XX 10-AUG-2000 (first entry)
XX
XX Human bone marrow-derived serum protein 1.
XX
XX Bone marrow-derived serum protein; immunoglobulin kappa light chain;
XX BMDSP-1; cytostatic; anti-HIV; antiasthmatic; antithrombotic;
XX anti-inflammatory; antirheumatic; antisclerotic; hypotensive; antiviral;
XX antiparasitic.
XX
XX Homo sapiens.
OS
XX

Key Location/Qualifiers
FH 18
FT Modified-site /note= "potential casein kinase II phosphorylation site"
FT Modified-site 34 /note= "potential casein kinase II phosphorylation site"
FT Domain 36..110 /label= "immunoglobulin_domain"
FT Modified-site 42 /note= "potential protein kinase C phosphorylation site"
FT Modified-site 72 /note= "potential protein kinase C phosphorylation site"
FT Modified-site 87 /note= "potential protein kinase C phosphorylation site"
FT Modified-site 96 /note= "potential casein kinase II phosphorylation site"
FT Modified-site 122 /note= "potential casein kinase II phosphorylation site"
FT Domain 147..216 /label= "immunoglobulin_domain"
FT Domain 151..173 /label= "immunoglobulin_domain"
FT Domain /label= "immunoglobulin"
FT Modified-site 182 /note= "potential casein kinase II phosphorylation site"
FT Modified-site 184 /note= "potential casein kinase II phosphorylation site"
FT Domain 190..233 /label= "immunoglobulin"
FT Modified-site 202 /note= "potential casein kinase II phosphorylation site"
FT Domain 212..229 /label= "immunoglobulin"
FT /note= "immunoglobulin"
XX
XX WO2000020588-A2.
XX
XX 13-APR-2000.
XX

PF 01-OCT-1999; 99WO-US222908.
XX
XX 02-OCT-1998; 98US-0165621.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Tang YT, Corley NC, Guegler KJ, Lu DAM;
XX
XX
XX

DR WPI: 2000-303775/26.
XX
XX N-PSDB: A09154.
XX

PT Purified polypeptide for treating or preventing disorders associated
PT with decreased expression or activity of bone marrow-derived serum
PT proteins
XX
XX

PS Claim 1: Page 68-69; 72pp; English.

XX Human bone marrow-derived serum proteins (BMDSP) 1 has chemical and
XX structural similarity with immunoglobulin kappa light chain. BMDSP-1
XX and BMDSP-2 are useful for treating or preventing a disorder associated
XX with decreased expression or activity of BMDSP.
XX Antagonists of BMDSP are useful for treating or preventing a disorder
XX associated with increased expression or activity of bone marrow-derived
XX serum proteins. The disorders include cancers (melanoma, adenocarcinoma,
XX sarcoma), immune disorders (acquired immunodeficiency syndrome (AIDS),
XX asthma, atherosclerosis, Crohn's disease, bronchitis, multiple sclerosis,
XX osteo- and rheumatoid arthritis), viral infections, parasitic infections
XX (schistosoma, tapeworm), and vascular disorders (arteriosclerosis,
XX hypertension, vasculitis).
XX
XX Sequence 234 AA:
SQ

Query Match 83.0%; Score 510.5; DB 21; Length 234;
Best Local Similarity 85.5%; Pred. No. 1.7e-30;
Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LWPDPITGEIVMTOSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGCAPRLIYGAS 60
DB 13 LWPDPITGEIVMTOSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGCAPRLIYGAS 72
OY 61 TRATGIPARFSGSGSTEFTLTSSLSQSDPAVYCYQOYNNMPP-YTFGGCKLEIK 117
DB 73 nratgiparfsgsgstgdflltsslepedfayycqyft-tpytfggtrleikr 128

RESULT 11

ID Y06842
XX Y06842 standard; Protein: 214 AA.

AC Y06842;
XX
XX 25-JUN-1999 (first entry)
XX
XX
XX Seq ID No:10 of JP11089576.
XX
XX

KW AntiHBs; monoclonal antibody; Epstein Barr virus; EBV; adr type;
KW human; HBs antigen; hepatitis C.
XX
XX

OS Homo sapiens.
XX
XX

PN JP11089576-A.
XX
XX

PD 06-APR-1999.
XX
XX

PF 19-SEP-1997; 97JP-0255705.
XX
XX

PR 19-SEP-1997; 97JP-0255705.
XX
XX

PA (N1SN) NISSHINBO IND INC.
XX
XX

DR WPI: 1999-281053/24.
XX
XX

DR N-PSDB: X32826.
XX

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XX Anti-HBs monoclonal antibody - produced without the risk of Epstein
PT Barr virus contamination
XX
XX Disclosure: Page 9-10; 12pp; Japanese.
XX
CC The invention relates to an antiHBs monoclonal antibody having the
CC following properties: (A) CDR-3 of H chain variable region; (B) it
CC contains no Epstein Barr virus (EBV); (C) it binds at least one adr type
CC among human HBs antigens. The antiHBs monoclonal antibody is high in
CC antibody titer and has low risk of EBV contamination. It can be used to
CC prevent hepatitis C.
XX
SQ Sequence 214 AA:

Query Match 82.8%; Score 509.5; DB 20; Length 214;
Best Local Similarity 93.6%; Pred. No. 1.9e-30;
Matches 102; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 68
DB 1 elvmtqspatlsvspgeratlscrasqsvrnlawyqkpgqaprllyaastratgipa 60
QY 69 RFGSGSGSEFTLTLSLQSEDFAVYYCCQYNNMPYTFGQGTLEIKR 117
DB 61 rfgsgsgseftltlsslqsedfavyccqynnew-frtfggtkveikr 108

RESULT 12
W1155
ID W1155 standard; Protein: 134 AA.
XX
XX W1155;
AC
XX
XX 14-MAY-1997 (first entry)
DT
XX
XX Anti-lung tumour antigen monoclonal antibody light chain.
DE
XX
XX Light chain monoclonal; antibody; TB2A36C3; lung; tumour; EBV;
KM Epstein-Barr virus; TB945; human; B cell; screen; antigen;
KM carcinoma; lysis; anti-tumour therapy; activation; CD4; CD8;
XX cell.
XX
XX Homo sapiens.
OS
XX
XX WO9628473-A1.
PN
XX
XX 19-SEP-1996.
PD
XX
XX 18-MAR-1996; 96WO-US03661.
PF
XX
XX 16-MAR-1995; 95US-0405034.
PR
XX
XX (MEDE/) MEDENICA R D.
PA
XX
XX Mukerjee S;
PI
XX
XX WPI: 1996-433764/43.
DR
XX
XX N-PSDB: T33664.
DR
XX
XX Anti-lung tumour antigen monoclonal antibody TB2A36C3 - produced by
PT Epstein-Barr virus transformation of human lung cancer patient
PT B-cells, useful in conjunction with other agents for lysis of
PT tumours
XX
XX Claim 12; Page 25; 46pp; English.
XX
XX The present sequence is the light chain from the monoclonal
CC antibody (MAB) TB2A36C3, which has high specificity against lung
CC tumour antigens and is produced by an Epstein-Barr virus (EBV)
CC transformed T9945 human B cell line. The MAB can be used to screen
CC serum or tissue samples for a carcinoma associated antigen, lyse

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CC tumours in anti-tumour therapy (optionally with other agents) and
CC activate immune competent CD4 or CD8 cells in a patient's blood
CC system.
CC Tumour draining lymph nodes obtained from a non-SCIC (small cell
CC lung cancer) patient were cut into fine pieces and washed. Pure B
CC cells, isolated using CD19 coated immunomagnetic beads, were
CC immortalised by EBV transformation, and plated and assayed for
CC activity. Clones which showed positive reactivity with autologous
CC tumour cells from the patient and the SCIC cell line NCIM69, were
CC subjected to limiting dilution to prepare the MAb.
XX
SQ Sequence 134 AA:

Query Match 82.0%; Score 504.5; DB 17; Length 134;
Best Local Similarity 84.7%; Pred. No. 2.8e-30;
Matches 100; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 LMLPDTGEIVMTQSPATLSVSPGERATLSCRASQSVS-SNLAWYQKPGQAPRLLIYGA 59
DB 13 lmlpdtgeivltqspatlsvspgeratlscrasqsvsfrslawyqkpgqapsllyga 72
QY 60 STRATGIPARFSGSGSGTEFTLTLSLQSEDFAVYYCCQYNNMPYTFGQGTLEIKR 117
DB 73 stratgipdrfsgsgsgtdltlsslqsedfavyccqygsaarylfggtkveikr 130

RESULT 13
R41286
ID R41286 standard; Protein: 129 AA.
XX
XX R41286;
AC
XX
XX 01-NOV-1993 (first entry)
DT
XX
XX F105 rearranged variable region light chain.
DE
XX
XX Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS;
KM CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KM chain; epitope; immune deficiency.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= sig_peptide
FT Protein 20..129
FT /label= mat_protein
XX
XX WO9312232-A.
PN
XX
XX 24-JUN-1993.
PD
XX
XX 10-DEC-1992; 92WO-US10928.
PF
XX
XX 10-DEC-1991; 91US-0804652.
PR
XX
XX (DAND ) DANA FARBER CANCER INST INC.
PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
XX
XX Haseltine WA, Marasco WA, Posner MR, Sotiroski JG;
PI
XX
XX WPI: 1993-214174/26.
DR
XX
XX N-PSDB: Q49155.
DR
XX
XX DNA segments encoding monoclonal antibody - which binds to gp120
PT and neutralises HIV, for treating AIDS, and for diagnosing and
PT monitoring HIV infection
XX
XX Claim 10; Page 79; 109pp; English.
XX
XX mRNA from the known hybridoma F105 was converted to cDNA and this
CC subjected to PCR amplification using primers corresp. to appropriate

```

CC parts of the heavy or light chains and having restriction sites to permit cloning. The extension prods. were isolated and sequenced.
 CC The recombinant human monoclonal antibody (MAb) binds to a
 CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
 CC the binding of gp120 to the CD4 receptor, and neutralises a broad
 CC range of HIV isolates. The MAb may be used to treat immune
 CC deficiency, esp. at doses of 0.1-10 mg/kg.

Sequence 129 AA:

Query Match 81.1%; Score 499; DB 14; Length 129;
 Best Local Similarity 84.7%; Pred. No. 6,8e-30;
 Matches 100; Conservative 7; Mismatches 9; Indels 2; Gaps 2;

OY 1 LMLPDTGIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMVQOKPGQAPRLIIYGA 59
 |||
 Db 13 Lwlpdtgtelvtlqspgtltslaseratlscrasgsvsrslawyqkpgqaprliliyga 72
 OY 60 STRATGIPARFSGSGGTEFTLTISLSQSEDFAVVYCCQYNNMPPYTFGQGTKEIKR 117
 |||
 Db 73 sratgipdrfsgsggtfdltltsrvepedfavyycqgdn-svctfsggtkleikr 129

RESULT 14

R38673 R38673 standard; Protein; 129 AA.

AC R38673;

DT 01-NOV-1993 (first entry)

DE F105VK-F105JK.

KM Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;
 KM CD4 receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KM chain; epitope; immune deficiency.

OS Homo sapiens.

FT Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein 21..129

FT Region 1..116
 FT Region 117..129

FT Region 117..129

FT Region 44..55

FT Region 71..77

FT Region 110..117

FT Region 110..117

FT Region 110..117

FT Region 110..117

FT Region 110..117

FT Region 110..117

FT Region 110..117

FT Region 110..117

FT Region 110..117

FT Region 110..117

FT Region 110..117

FT Region 110..117

XX 10-DEC-1991; 91US-0804652.

PR (DAND) DANA FARBER CANCER INST INC.

PA (NEW) NEW ENGLAND DEACONNESS HOSPITAL CORP.

PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;

DR WPI: 1993-214174/26.

DR N-PSDB; Q42706.

PT DNA segments encoding monoclonal antibody - which binds to gp120

PT and neutralises HIV, for treating AIDS, and for diagnosing and

PT monitoring HIV infection

PS Disclosure; Page 74-75; 109pp; English.

CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from

CC other F105 VK sequences given elsewhere in the specification) was

CC compared with germline gene HumvK325 (Q42706), showing 97.7%

CC similarity. By nucleotide sequence analysis, F105 appears to

CC be derived from a member of the VK III subgroup gene family.

XX Sequence 129 AA:

Query Match 80.8%; Score 497; DB 14; Length 129;
 Best Local Similarity 84.7%; Pred. No. 9,5e-30;
 Matches 100; Conservative 7; Mismatches 9; Indels 2; Gaps 2;

OY 1 LMLPDTGIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMVQOKPGQAPRLIIYGA 59
 |||
 Db 13 Lwlpdtgtelvtlqspgtltslaseratlscrasgsvsrslawyqkpgqaprliliyga 72

OY 60 STRATGIPARFSGSGGTEFTLTISLSQSEDFAVVYCCQYNNMPPYTFGQGTKEIKR 117
 |||
 Db 73 sratgipdrfsgsggtfdltltsrvepedfavyycqgdn-svctfsggtkleikr 129

RESULT 15

W40069 W40069 standard; Protein; 150 AA.

AC W40069;

DT 29-MAY-1998 (first entry)

DE Human monoclonal antibody H11 protein variable region H chain.

DE H11; monoclonal antibody; MAb; C-antigen; variable region heavy chain;

DE V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;

DE primer; vaccine; gene therapy; glioblastoma; neuroblastoma;

DE malignant melanoma; adenocarcinoma; small cell lung carcinoma.

OS Homo sapiens.

OS Homo sapiens.

OS Homo sapiens.

OS Homo sapiens.

OS Homo sapiens.

OS Homo sapiens.

OS Homo sapiens.

Antigen binding fragment from monoclonal antibody, H11 - allows
 tumour specific detection and treatment of neoplasia

XX Claim 1; Page 87-88; 126pp; English

CC This sequence represents the human H11 monoclonal antibody variable (V)
CC region heavy (H) chain which specifically recognises the C-antigen. Such
CC an antigen binding fragment may be used for treating a patient with
CC leukaemia. It is especially useful in the detection of lymphomas and
CC leukaemia where the tumour cells bearing the C antigen are circulating
CC in the patients bloodstream. The polynucleotide sequence may be used as a
CC primer or a probe and the encoded protein may be used in a vaccine or
CC for gene therapy. The human monoclonal antibody (Mab), designated H11,
CC specifically recognises cancerous cells. H11 is specific for
CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,
CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
CC prostate adenocarcinoma. The antigen binding fragment may also be used
CC to detect C-antigen in a sample.

SQ Sequence 150 AA;

Query Match	80.3%;	Score 494;	DB 19;	Length 150;
PostgreSQL	81.0%;	Score 494;	DB 19;	Length 150;

Best Local Similarity	81.06;	Prod. NO. 1.8e+29;							
Matches	98;	Conservative	9;	Mismatches	10;	Indels	4;	Gaps	2;

Oy	1	LMLPDTTEIYMTPSPALISVSPERATLSICRAQSIVSN--LAWYQOKPCOAPLLTYGA	59
Db	17	lwlpldtgdvltqspgltlsperatllscraasqvssaylawyqqkpgqpalllyga	76
Oy	60	STRANGIPARESGSGSTEFPLTITSSLOSSEDFAYYYCOOYN--WPPYFEGGTREIK	116
Db	77	stratgmprtsqsgsdclftlslrlepedfayyycqgysspqtqptciftgskveik	136
Oy	117	R	117
Db	137	r	137

Search completed: March 9, 2001, 16:43:36
Job time: 35 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2001, 16:44:01 ; Search time 23.59 seconds
(without alignments)
336.769 Million cell updates/sec

Title: US-09-203-768a-4

Perfect score: 615

Sequence: 1 LMLPDTTGEIVMTQSPATLS.....QYNNMPPTFGGQTKLEIKR 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir66:*
2: pir1:*
3: pir2:*
4: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	95.7	128	S40343	Ig kappa chain V-J
2	574.5	93.4	117	S40362	Ig kappa chain - h
3	562	91.4	131	S40328	Ig kappa chain - h
4	539.5	87.7	123	S40378	Ig kappa chain - h
5	530.5	86.3	128	A56701	Ig kappa chain V r
6	527	85.7	115	K3HUC1	Ig kappa chain pre
7	526.5	85.6	107	S34005	Ig kappa chain V r
8	526	85.5	115	A30553	Ig kappa chain pre
9	525.5	85.4	144	PI0106	Ig kappa chain pre
10	523	85.0	116	B26555	Ig kappa chain V-I
11	522	84.9	110	S40326	Ig kappa chain V-J
12	518.5	84.3	128	S40379	Ig kappa chain V-J
13	514	83.6	215	JEO244	Ig kappa chain NIg
14	513.5	83.5	129	S29627	Ig kappa chain V r
15	511.5	83.2	114	S46375	Ig kappa chain V-J
16	510	82.9	129	K3HUA	Ig kappa chain pre
17	510	82.9	129	S49532	Ig kappa chain V r
18	510	82.9	134	S38643	Ig kappa chain V r
19	510	82.9	134	S38643	Ig kappa chain V r
20	509.5	82.8	128	S40345	Ig kappa chain V-J
21	509	82.8	129	K3HUI	Ig kappa chain pre
22	505	82.1	108	S40377	Ig kappa chain - h
23	504	82.0	109	K3HUPM	Ig kappa chain V-I
24	502	81.6	129	A33274	Ig kappa chain pre
25	499	81.1	128	S20636	Ig kappa chain V r
26	498	81.0	130	S20637	Ig kappa chain V r
27	496	80.7	114	S54905	Ig kappa chain V r
28	496	80.7	130	S40360	Ig kappa chain - h
29	494	80.3	129	S40363	Ig kappa chain - h

30	493.5	80.2	128	1	K3HUA1	Ig kappa chain pre
31	492.5	80.1	131	2	S40346	Ig kappa chain V-J
32	490.5	79.8	111	2	S23628	Ig kappa chain V r
33	489.5	79.6	125	2	S40344	Ig kappa chain V-J
34	489	79.5	115	1	K3HUC	Ig kappa chain pre
35	485.5	78.9	129	2	S40325	Ig kappa chain - h
36	485	78.9	121	2	S40327	Ig kappa chain - h
37	484	78.7	124	2	S20633	Ig kappa chain - h
38	482.5	78.5	215	2	JEO243	Ig kappa chain NIg
39	479.5	78.0	119	2	S41816	Ig kappa chain V r
40	478	77.7	98	2	I30608	Ig kappa chain V-I
41	476	77.4	95	2	PH0868	Ig kappa chain V-I
42	475	77.2	109	2	H30601	Ig kappa chain V-I
43	471.5	76.7	108	2	G44151	Ig kappa chain V r
44	467	75.9	145	2	S20631	Ig kappa chain - h
45	465	75.6	108	2	C30608	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
S40343
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40343
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40343
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: EMBL:X72453; NID:g441374; PIDN:CAA51121.1; PID:g441375
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 588.5; DB 2; Length 128;
Best Local Similarity 97.4%; Pred. No. 5e-42;
Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 LMLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLITYGAS 60
Db 13 LMLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLITYGAS 72
QY 61 TRATGIPARFSGSGSTTEFTLTISLSQSEDFAYVYCOQYNNMPPTFGGQTKLEIKR 117
Db 73 TRATGIPARFSGSGSTTEFTLTISLSQSEDFAYVYCOQYNNMPPTFGGQTKLEIKR 128

RESULT 2
S40362
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40362
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40362
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <KLE>
A:Cross-references: EMBL:X72472; NID:g441412; PID:g441413
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 574.5; DB 2; Length 117;
Best Local Similarity 96.6%; Pred. No. 6, 6e-41;
Matches 112; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
|||||
DB 3 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 62
|||||

OY 61 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIK 116
|||||
DB 63 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIK 117
|||||

RESULT 3
S40328
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40328
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40328
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72438; NID:g441344; PIDN:CA451106.1; PID:g441345
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-109/Domain: Immunoglobulin homology <IMM>

Query Match 91.4%; Score 562; DB 2; Length 131;
Best Local Similarity 89.7%; Pred. No. 7, 9e-40;
Matches 105; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
|||||
DB 12 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAY 71
|||||

OY 61 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 117
|||||
DB 72 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 128
|||||

RESULT 4
S40378
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40378
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40378
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72488; NID:g441444; PIDN:CA451156.1; PID:g441445
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:29-103/Domain: Immunoglobulin homology <IMM>

Query Match 87.7%; Score 539.5; DB 2; Length 123;
Best Local Similarity 87.3%; Pred. No. 5, 3e-38;
Matches 103; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
|||||

DB 6 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 65
OY 61 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 117
|||||
DB 66 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 123
|||||

RESULT 5
A56701
Ig kappa chain V region precursor (Hua) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: A56701
R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A:Title: Human and mouse monoclonal antibodies to blood group A substance, which are
A:Reference number: A56701; MUID:95279371
A:Accession: A56701
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <NIC>
A:Cross-references: GB:IA1174; NID:9762823; PIDN:AA64877.1; PID:9762824
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: Immunoglobulin homology <IMM>

Query Match 86.3%; Score 530.5; DB 2; Length 128;
Best Local Similarity 88.0%; Pred. No. 3e-37;
Matches 103; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
|||||
DB 13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYDAS 72
|||||

OY 61 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 117
|||||
DB 73 NRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 128
|||||

RESULT 6
K3HUC1
Ig kappa chain precursor V-III region (CLL) - human
N:Alternate names: Rheumatoid factor
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
C:Accession: A01898
R:Jirik, F.R.; Sorge, J.; Fong, S.; Heltmann, J.G.; Curo, J.G.; Chen, P.P.; Goldfien
Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
A:Title: Cloning and sequence determination of a human rheumatoid factor light-chain
A:Reference number: A01898; MUID:86177570
A:Accession: A01898
A:Molecule type: DNA
A:Residues: 1-115 <JIR>
A:Note: The sequence was determined from the germline gene
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chain disulfide bonds. In some cases, such as IGA and IGH, the subunits associate into C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:1-20/Domain: Signal sequence #status predicted <SIG>
F:21-115/Product: Rheumatoid factor, Ig kappa chain V-III region (CLL) #status predicted
F:21-43/Region: framework 1
F:36-110/Domain: Immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:55-69/Region: framework 2
F:70-76/Region: complementarity-determining 2
F:77-108/Region: framework 3
F:109-115/Region: complementarity-determining 3

F:43-108/Disulfide bonds: #status predicted

Query Match 85.7%; Score 527; DB 1; Length 115;
Best Local Similarity 97.1%; Pred. No. 5.3e-37;
Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LMLPDTTGEIVMQSPATILSVSPGERATLSCRASQSVSNLAWYQQRPGQAPRLIYGAS 60
|||||
DB 13 LMLPDTTGEIVMQSPATILSVSPGERATLSCRASQSVSNLAWYQQRPGQAPRLIYGAS 72
QY 61 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMP 103
|||||
DB 73 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMP 115

RESULT 7
S34005
Ig kappa chain V region - human

C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34005; S30524
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281
A:Accession: S34005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <MAR>
A:Cross-references: EMBL:Z18330
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 526.5; DB 2; Length 107;
Best Local Similarity 96.3%; Pred. No. 5.5e-37;
Matches 104; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 EIVMQSPATILSVSPGERATLSCRASQSVSNLAWYQQRPGQAPRLIYGAS 68
|||||
DB 1 EIVMQSPATILSVSPGERATLSCRASQSVSNLAWYQQRPGQAPRLIYGAS 60
QY 69 RFGSGSGTEFTLTISLQSEDFAYVYCOQYNNMPYTGQTKLEIK 116
|||||
DB 61 RFGSGSGTEFTLTISLQSEDFAYVYCOQYNNMPYTGQTKLEIK 107

RESULT 8
A30553

Ig kappa chain precursor V-III region (Hab) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: A30553
R:Liu, M.F.; Robbins, D.L.; Crowley, J.J.; Sinha, S.; Kozin, F.; Kipps, T.J.; Carson, D.
J. Immunol. 142, 688-694, 1989
A:Title: Characterization of four homologous L chain variable region genes that are related
A:Reference number: A30553; MUID:89093959
A:Accession: A30553
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <LIU>
A:Note: the sequence was determined from the differentiated gene
C:Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 526; DB 2; Length 115;
Best Local Similarity 97.1%; Pred. No. 6.5e-37;
Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LMLPDTTGEIVMQSPATILSVSPGERATLSCRASQSVSNLAWYQQRPGQAPRLIYGAS 60
|||||
DB 13 LMLPDTTGEIVMQSPATILSVSPGERATLSCRASQSVSNLAWYQQRPGQAPRLIYGAS 72
QY 61 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMP 103
|||||
DB 73 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMP 115

RESULT 9
P10106

Ig kappa chain precursor V-J-C region (LSI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: P10106
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma
A:Reference number: P10106; MUID:8923583
A:Accession: P10106
A:Molecule type: mRNA
A:Residues: 1-144 <SIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-110/Domain: V region <VRE>
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match 85.4%; Score 525.5; DB 2; Length 144;
Best Local Similarity 87.2%; Pred. No. 8.8e-37;
Matches 102; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 LMLPDTTGEIVMQSPATILSVSPGERATLSCRASQSVSNLAWYQQRPGQAPRLIYGAS 60
|||||
DB 13 LMLPDTTGEIVMQSPATILSVSPGERATLSCRASQSVSNLAWYQQRPGQAPRLIYGAS 72
QY 61 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMPYTGQTKLEIK 117
|||||
DB 73 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMPYTGQTKLEIK 128

RESULT 10
B26555

Ig kappa chain V-III region (Ger) - human
C:Species: Homo sapiens (man)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26555
R:Middleton, C.R.; Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A:Title: Atycyl glycosylation of an IgG monoclonal cryoimmunoglobulin.
A:Reference number: A92630; MUID:87137666
A:Accession: B26555
A:Molecule type: protein
A:Residues: 1-116 <MID>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 523; DB 2; Length 116;
Best Local Similarity 91.7%; Pred. No. 1.1e-36;
Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 9 EIVMQSPATILSVSPGERATLSCRASQSVSNLAWYQQRPGQAPRLIYGAS 68
|||||
DB 1 EIVMQSPATILSVSPGERATLSCRASQSVSNLAWYQQRPGQAPRLIYGAS 60

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re-
A:Reference number: S46369; MUID:94313975
A:Accession: S46375
A:Molecule type: mRNA
A:Residues: 1-114 <BEN>
A:Cross-references: EMBL:Z27176; NID:9415967; PIDN:CA81700.1; PID:9415968
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:20-95/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 511.5; DB 2; Length 114;
Best Local Similarity 86.8%; Pred. No. 1e-35;
Matches 99; Conservative 8; Mismatches 6; Indels 1; Gaps 1;
OY 5 DTGELIVMTOSPATLSVSPGERATLSCRASQSVSSN-LAWYOOKPGQAPRLITYGASTRA 63
Db 1 DTGELIVLTOSPCTLSLSPGERATLSCRASQSISSYLAWYQOKPGQAPRLITYGASSRA 60
OY 64 TGIPIARFSSGSGTEFTLTITSSIQSEDFAVYYCQYNNMPPTTFGGGTKLEIKR 117
Db 61 TGIPIARFSSGSGSGTDEFTLTITISRLPEDFAVYYCQYGGSSPPTTFGGGTKLEIKR 114

Search completed: March 9, 2001, 16:44:01
Job time: 60 sec

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OY 61 TRATGIPARFSSGSGTEFTLTISLQSEDFAVYVCOQYNNMPPYFGQTKLEIKR 117
 |||||||
 DB 73 TRATGIPARFSSGSGTEFTLTISLQSEDFAVYVCOQYNNMPPYFGQTKLEIKR 129

RESULT 2

KV3L_HUMAN STANDARD; PRT; 129 AA.
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88171307; PubMed-3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.

DR PIR: P10022; K3HUPH.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL
 FT CHAIN 1 20
 FT DOMAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 82.9%; Score 510; DB 1; Length 129;
 Best Local Similarity 85.6%; Pred. No. 7.2e-43;
 Matches 101; Conservative 7; Mismatches 8; Indels 2; Gaps 2;

OY 1 LMLPPTGIVMTGSPATISVSGERATLSCRASOSVSSN-LAWYQKQGAAPRLIITYGA 59
 |||||||
 DB 13 LMLPPTGIVMTGSPATISVSGERATLSCRASOSVSSYLAWYQKQGAAPRLIITYGA 72
 |||||||
 OY 60 STRATGIPARFSSGSGTEFTLTISLQSEDFAVYVCOQYNNMPPYFGQTKLEIKR 117
 |||||||
 DB 73 SSRATGIPDRFSGSGSGTFTLTISRLPEDEPAVYVCOQYGN-SPRTFQGTKEIKR 129

RESULT 3

KV3M_HUMAN STANDARD; PRT; 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88171307; PubMed-3127527;

RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.

DR PIR: P10021; K3HUPH.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL
 FT CHAIN 1 20
 FT DOMAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B874D6 CRC64;

Query Match 82.8%; Score 509; DB 1; Length 129;
 Best Local Similarity 84.7%; Pred. No. 9e-43;
 Matches 100; Conservative 9; Mismatches 7; Indels 2; Gaps 2;

OY 1 LMLPPTGIVMTGSPATISVSGERATLSCRASOSVSSN-LAWYQKQGAAPRLIITYGA 59
 |||||||
 DB 13 LMLPPTGIVMTGSPATISVSGERATLSCRASOSVSSYLAWYQKQGAAPRLIITYGA 72
 |||||||
 OY 60 STRATGIPARFSSGSGTEFTLTISLQSEDFAVYVCOQYNNMPPYFGQTKLEIKR 117
 |||||||
 DB 73 SSRATGIPDRFSGSGSGTFTLTISRLPEDEPAVYVCOQYGN-SPRTFQGTKEIKR 129

RESULT 4

KV3F_HUMAN STANDARD; PRT; 109 AA.
 AC P01624;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION POM.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-76276460; PubMed-60899;
 RA Klapper D.G., Capra J.D.;
 RT "The amino acid sequence of the variable regions of the light chains
 RT from two idiotypically cross reactive IGM anti-gamma globulins.";
 RL Ann. Immunol. (Paris) 127C:261-271(1976).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR: A01897; K3HUPM.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11922 MW; 62821DDCA8ABA86 CRC64;

Query Match 82.0%; Score 504; DB 1; Length 109;
 Best Local Similarity 90.9%; Pred. No. 2.3e-42;
 Matches 100; Conservative 4; Mismatches 4; Indels 2; Gaps 2;

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OY 9 EIVMTQSPATISVSPGERATISCRASQSVS-SNLAMYQKPGQAPRLIYGASTRATGIP 67
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 EIVMTQSPATISVSPGERATISCRASQSVS-SNLAMYQKPGQAPRLIYGASTRATGIP 60
OY 68 AFESSGSGTEFTLTISLSQSEDFAVYCCQYNNMPPTTFGGGTLEIKR 117
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 AFESSGSGTEFTLTISLSQSEDFAVYCCQYNNMP-TEGGGTVEIKR 109

RESULT 5
KV3K_HUMAN STANDARD: PRT: 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Melndi A., Combriato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III."
RL Nucleic Acids Res. 13:6499-6513(1985).
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DR EMBL: Z00021; CAA7316.1; -
DR PIR: A01899; K3H041.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1g.1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JKI SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0EE3B9012 CRC64;

Query Match 80.2%; Score 493.5; DB 1; Length 128;
Best Local Similarity 82.9%; Pred. No. 2.8e-41;
Matches 97; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

OY 1 LMLPDTGEIVTQSPATISVSPGERATISCRASQSVS-SNLAMYQKPGQAPRLIYGAS 60
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 13 LMLPDTGEIVTQSPATISVSPGERATISCRASQSVS-SNLAMYQKPGQAPRLIYDAS 72
OY 61 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYCCQYNNMPPTTFGGGTLEIKR 117
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 73 SRANGIPARFSSGSGTEFTLTISLSQSEDFAVYCCQYNNMP-SPYTFGGGTLEIKR 128

RESULT 6
KV3I_HUMAN STANDARD: PRT: 115 AA.
AC P04433;

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DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
-----
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CC or send an email to license@isb-sib.ch).
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DR EMBL: X01668; -, NOT_ANNOTATED_CDS.
DR PIR: A01900; K3H0VG.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1g.1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 79.5%; Score 489; DB 1; Length 115;
Best Local Similarity 90.3%; Pred. No. 6.9e-41;
Matches 93; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LMLPDTGEIVTQSPATISVSPGERATISCRASQSVS-SNLAMYQKPGQAPRLIYGAS 60
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 13 LMLPDTGEIVTQSPATISVSPGERATISCRASQSVS-SNLAMYQKPGQAPRLIYDAS 72
OY 61 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYCCQYNNMP 103
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 73 NRATGIPARFSSGSGTEFTLTISLSQSEDFAVYCCQYNNMP 115

RESULT 7
KV3J_HUMAN STANDARD: PRT: 116 AA.
AC P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION VH PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RT within the VK locus."
RL Nucleic Acids Res. 12:9229-9236(1984).
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DR EMBL: X02725; -- NOT_ANNOTATED_CDS.

DR PIR: A01901; K3HUVH.

DR HSSP: P01789; 2MCP.

DR INTERPRO: IPR003006; --

DR PFAM: PF00047; 1g; 1.

DR KAPPA CHAIN V-III REGION. Signal.

FT CHAIN 1 20

FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.

FT DOMAIN 1 43 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 56 70 FRAMEWORK 2.

FT DOMAIN 71 77 FRAMEWORK 2.

FT DOMAIN 78 109 FRAMEWORK 3.

FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3.

FT DISULFID 43 109 BY SIMILARITY.

FT NON_TER 116 116

SO SEQUENCE 116 AA: 12757 MW: 51CD55BA53B21929 CRC64;

Query Match 74.6%; Score 458.5; DB 1; Length 116;

Best Local Similarity 87.5%; Pred. No. 6.2e-38;

Matches 91; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

1 LMLPDTGEIVWTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQOKPGQAPRLIYGA 59

13 LMLPDTGEIVWTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQOKPGQAPRLIYGA 72

60 STRATGIPARFSGSGTDEFTLTISLQSEDFAVYCCQYNNMP 103

73 STRATGIPARFSGSGTDEFTLTISLQSEDFAVYCCQYNNMP 116

RESULT 8

KV3B_HUMAN STANDARD; PRT; 109 AA.

AC P01620;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

IG KAPPA CHAIN V-III REGION SITE.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

SEQUENCE.

MEDLINE-82046598; PubMed-6794615;

Andrews D.W., Capra J.D.;

"Amino acid sequence of the variable regions of light chains from two

idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa

group."

Biochemistry 20:5816-5822(1981).

-1 MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

GLOBULIN ACTIVITY.

PIR: A01892; K3HUSI.

HSSP: P01789; 2MCP.

INTERPRO: IPR003006; --

PFAM: PF00047; 1g; 1.

Immunoglobulin V region.

DISULFID 23 89

NON_TER 109 109 BY SIMILARITY.

SEQUENCE 109 AA: 11775 MW: 7689C3EC6D646FFB4 CRC64;

Query Match 73.8%; Score 454; DB 1; Length 109;

Best Local Similarity 82.7%; Pred. No. 1.6e-37;

Matches 91; Conservative 9; Mismatches 8; Indels 2; Gaps 2;

9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQOKPGQAPRLIYGA STRATGIP 67

1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSN-LAMYQOKPGQAPRLIYGA STRATGIP 60

68 ARFSSGSGTDEFTLTISLQSEDFAVYCCQYNNMPYTFGGTLEIKR 117

61 DRFSSGSGTDEFTLTISLQSEDFAVYCCQYNNMPYTFGGTLEIKR 109

RESULT 9

KV3D_HUMAN STANDARD; PRT; 109 AA.

AC P01622;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

IG KAPPA CHAIN V-III REGION TI.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

SEQUENCE.

MEDLINE-72188439; PubMed-5027703;

Suter L., Barnikol H.U., Matanabe S., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal

immunoglobulin I-chain of kappa-type, subgroup 3 (Bence-Jones protein

TI). IV. The complete amino acid sequence and its significance for

the mechanism of antibody production."

Hoppe-Seiler's Z. Physiol. Chem. 353:189-208(1972).

-1 MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-1 MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

PIR: A01895; K3HUTI.

HSSP: P01789; 2MCP.

INTERPRO: IPR003006; --

PFAM: PF00047; 1g; 1.

Immunoglobulin V region; Bence-Jones protein.

DISULFID 23 89 BY SIMILARITY.

NON_TER 109 109

SEQUENCE 109 AA: 11788 MW: 8C35058C8C7749BC CRC64;

Query Match 73.0%; Score 449; DB 1; Length 109;

Best Local Similarity 81.8%; Pred. No. 4.8e-37;

Matches 90; Conservative 10; Mismatches 8; Indels 2; Gaps 2;

9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQOKPGQAPRLIYGA STRATGIP 67

1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSN-LAMYQOKPGQAPRLIYGA STRATGIP 60

68 ARFSSGSGTDEFTLTISLQSEDFAVYCCQYNNMPYTFGGTLEIKR 117

61 DRFSSGSGTDEFTLTISLQSEDFAVYCCQYNNMPYTFGGTLEIKR 109

RESULT 10

KV3E_HUMAN STANDARD; PRT; 109 AA.

AC P01623;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

IG KAPPA CHAIN V-III REGION WOL.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

SEQUENCE.

MEDLINE-82046598; PubMed-6794615;

Andrews D.W., Capra J.D.;

"Amino acid sequence of the variable regions of light chains from two

idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa

RT group."
 RT Biochemistry 20:5816-5822(1981).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR: A01896; K3HUML.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 KM Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109 BY SIMILARITY.
 SQ SEQUENCE 109 AA; 11746 MW; 566C115B69CEEE CRC64;

Query Match 72.8%; Score 448; DB 1; Length 109;
 Best Local Similarity 82.7%; Pred. No. 6, 1e-37;
 Matches 91; Conservative 7; Mismatches 10; Indels 2; Gaps 2;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 67
 DB 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSSGYLGWYQOKPGQAPRLIYGASTRATGIP 60
 OY 68 ARFSSGSGTEFTLTITSSLOSEDFAVYCOQYNNMPYTFGGTKLEIKR 117
 DB 61 DRFSSGSGTDFLTITSLRLEPEDFAVYCOQYGLS-GRTFGGTKVEIKR 109

RESULT 11
 KV3A_HUMAN STANDARD; PRT; 108 AA.
 AC P01619;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION B6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE.
 RA Milstein C.;
 RT "The basic sequences of immunoglobulin kappa chains: sequence studies
 RT of Bence Jones proteins Rad, F₁ and B₆."
 RL FEBS Lett. 2:301-304(1969).
 CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01891; K3HUB6.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match 71.5%; Score 440; DB 1; Length 108;
 Best Local Similarity 77.1%; Pred. No. 3, 6e-36;
 Matches 84; Conservative 13; Mismatches 10; Indels 2; Gaps 2;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 67
 DB 1 ZIVLTZSPGTLISLSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 60
 OY 68 ARFSSGSGTEFTLTITSSLOSEDFAVYCOQYNNMPYTFGGTKLEIKR 116
 DB 61 DRFSSGSGTDFLTITSLRLEPEDFAVYCOQYGLS-SPTFGGSGKLEIKR 108

RESULT 12
 KV1M_HUMAN STANDARD; PRT; 108 AA.
 AC P01605;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION IAY.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE.
 RA MEDLINE-77038198; PubMed-824717;
 RA Capra J.D., Klapper D.G.;
 RT "Complete amino acid sequence of the variable domains of two human
 RT Igm anti-gamma globulins (Iay/Pom) with shared idiotypic
 RT specificities."
 RT Scand. J. Immunol. 5:677-684(1976).
 CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
 CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
 CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR: A01871; K1HULY.
 DR HSSP: P01607; 1REL.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 2 34
 FT DOMAIN 3 49
 FT DOMAIN 4 56
 FT DOMAIN 5 57
 FT DOMAIN 6 58
 FT DOMAIN 7 88
 FT DOMAIN 8 97
 FT DOMAIN 9 107
 FT DISULFID 23 88
 FT NON_TER 108 108 BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 70.8%; Score 435.5; DB 1; Length 108;
 Best Local Similarity 73.4%; Pred. No. 9, 7e-36;
 Matches 80; Conservative 16; Mismatches 12; Indels 1; Gaps 1;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 68
 DB 1 DIQMTQSPSLSVSDRYTITTCQASQNNVAYLWYQOKPGQAPRLIYGASTRATGIP 60
 OY 69 RFSSGSGTEFTLTITSSLOSEDFAVYCOQYNNMPYTFGGTKLEIKR 117
 DB 61 RFSGSGSGTDFLTITSLRLEPEDIAITYCOQYNNMP-TFGGKTYEYKR 108

RESULT 13
 KV4C_HUMAN STANDARD; PRT; 134 AA.
 AC P06314;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86041854; PubMed-2997713;
 RA Marsh P., Mills F., Gould H.;
 RT "Detection of a unique human V kappa IV germline gene by a cloned
 RT cDNA probe."
 RT Nucleic Acids Res. 13:6531-6544(1985).
 RN [2]
 RP REVISION TO 76.
 RA Marsh P.;
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
 CC -----
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DR EMBL: X02990; CAA26733.1; -
 DR PIR: A01905; K4H017.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g; 1.
 DR Immunoglobulin V region; signal.
 FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 133 FRAMEWORK 4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 134 134
 SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 69.8%; Score 429.5; DB 1; Length 134;
 Best Local Similarity 69.9%; Pred. No. 4.7e-35;
 Matches 86; Conservative 16; Mismatches 14; Indels 7; Gaps 3;

OY 1 LMLPDTGEIYWTQSPATLSVSGERATLSGRASQSV--SSN---LAWYQOKPQOAPRL 54
 DB 13 LWSAGYDIIWVTPQSDSLAVSLGERATINCKSSQSLSSNNKMYLAWYQOKPQOAPRL 72
 OY 55 LIYGASTRATGIPARFSSGSGTEFTLTISLQSEDFAVYVYCOOYNNMPYTFGGGTLE 114
 DB 73 LIYMASTRESGVPRFSSGSGTEFTLTISLQAEADVAVYVYCOOYNNL-PWTFGGGTIVE 131
 OY 115 IKR 117
 DB 132 IKR 134

RESULT 14
 KV3G_HUMAN STANDARD; PRT: 109 AA.
 AC P04206;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION GOL (RHEUMATOID FACTOR).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE:86230578; PubMed:3086710;
 RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
 RT "Amino acid sequence of a light chain variable region of a human
 RT rheumatoid factor of the Wa idiotype group. In part predicted by its
 RT reactivity with anti-peptide antibodies";
 RL Mol. Immunol. 23:239-244(1986).
 DR PIR: A01893; K3HUGO.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g; 1.
 DR Immunoglobulin V region.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11830 MW; 9349A5BD93588B6 CRC64;

Query Match 69.6%; Score 428; DB 1; Length 109;
 Best Local Similarity 78.2%; Pred. No. 5.2e-35;
 Matches 86; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

OY 9 EIVMTQSPATLSVSGERATLSGRASQSV--SSN---LAWYQOKPQOAPRLIYGASTRATGIP 67
 DB 1 EIVLTQSPGTLISLSPGERATLSCRAALLSRGVLAWYQOKPQOAPRLIYGASTRATGIP 60
 OY 68 AFRSGSGTEFTLTISLQSEDFAVYVYCOOYNNMPYTFGGGTLEIKR 117
 DB 61 DRFSSGSGTEFTLTISLQAEADVAVYVYCOOYNGS-SPNSFGGTIVEIKR 109

RESULT 15
 KV4B_HUMAN STANDARD; PRT: 133 AA.
 ID P06313;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-IV REGION JI PRECURSOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:86041853; PubMed:2997712;
 RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mochkat R., Pohlenz H.D.,
 RA Zachau H.G.;
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
 RT single germline gene";
 RL Nucleic Acids Res. 13:6515-6529(1985).

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DR EMBL: Z00022; CAA77317.1; -
 DR PIR: A01904; K4H0J1.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 1g; 1.
 DR Immunoglobulin V region; signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 123 132 FRAMEWORK 4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 133 133
 SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 68.5%; Score 421; DB 1; Length 133;
 Best Local Similarity 69.9%; Pred. No. 3.1e-34;
 Matches 86; Conservative 15; Mismatches 14; Indels 8; Gaps 3;

OY 1 LMLPDTGEIYWTQSPATLSVSGERATLSGRASQSV--SSN---LAWYQOKPQOAPRL 54
 DB 13 LWSAGYDIIWVTPQSDSLAVSLGERATINCKSSQSLSSNNKMYLAWYQOKPQOAPRL 72
 OY 55 LIYGASTRATGIPARFSSGSGTEFTLTISLQSEDFAVYVYCOOYNNMPYTFGGGTLE 114
 DB 73 LIYMASTRESGVPRFSSGSGTEFTLTISLQAEADVAVYVYCOOYNNL-PWTFGGGTIVE 130

Fri Mar 9 16:49:13 2001

Qy	115	IKR	117
		111	
Db	131	IKR	133

Search completed: March 9, 2001, 16:46:05
Job time: 179 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2001, 16:46:47 ; Search time 38.3 Seconds
(without alignments)
358,050 Million cell updates/sec

Title: US-09-203-768a-4

Sequence: 1 LMLPDTGELVMTQSPATLS.....QYNMPPYFGQTKLEIKR 117

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529	86.0	109	4 Q9UL85	Q9UL85 homo sapien
2	513.5	83.5	108	4 Q9UL83	Q9UL83 homo sapien
3	449	73.0	109	4 Q9UL78	Q9UL78 homo sapien
4	431	70.1	109	4 Q9UL86	Q9UL86 homo sapien
5	425.5	69.2	108	4 Q9UL79	Q9UL79 homo sapien
6	394.5	64.1	108	4 Q9UL70	Q9UL70 homo sapien
7	390.5	63.5	108	4 Q9UL77	Q9UL77 homo sapien
8	378	61.5	107	4 Q9UL81	Q9UL81 homo sapien
9	357.5	58.1	298	11 Q9QYF0	Q9QYF0 mus musculu
10	352.5	57.3	114	4 Q9UL80	Q9UL80 homo sapien
11	347.5	56.5	214	11 Q9RIAS	Q9RIAS mus musculu
12	345	56.1	106	5 Q9UL10	Q9UL10 schistosoma
13	340.5	55.4	99	11 Q9UL74	Q9UL74 mus musculu
14	333.5	54.2	101	11 Q9UL78	Q9UL78 mus musculu
15	318.5	51.8	97	11 Q9UL76	Q9UL76 mus musculu
16	318.5	51.8	103	11 Q9UL80	Q9UL80 mus musculu
17	316.5	51.5	107	11 Q9UL84	Q9UL84 mus musculu
18	302	49.1	104	11 Q9UL82	Q9UL82 mus musculu
19	288.5	46.9	109	6 Q9N0W5	Q9N0W5 oryctolagus

20	242.5	39.4	107	4 Q9UL82	Q9UL82 homo sapien
21	231	37.6	107	4 Q9NSD6	Q9NSD6 homo sapien
22	219	35.6	130	4 Q9NP29	Q9NP29 homo sapien
23	151.5	24.6	93	4 Q9UL76	Q9UL76 homo sapien
24	145	23.6	123	11 Q61243	Q61243 mus musculu
25	143.5	23.3	123	4 Q9UK13	Q9UK13 homo sapien
26	134.5	21.9	119	4 Q9UL73	Q9UL73 homo sapien
27	131.5	21.4	116	4 Q9UL89	Q9UL89 homo sapien
28	128	20.8	109	11 Q9UL75	Q9UL75 mus musculu
29	125.5	20.4	320	13 Q9IAZ9	Q9IAZ9 spiroeroides
30	125	20.3	110	11 Q9UL77	Q9UL77 mus musculu
31	124.5	20.2	124	4 Q9UL92	Q9UL92 homo sapien
32	124	20.2	334	13 Q9IB05	Q9IB05 spiroeroides
33	124	20.2	337	13 Q9IB02	Q9IB02 spiroeroides
34	124	20.2	340	13 Q9IAZ6	Q9IAZ6 spiroeroides
35	123.5	20.1	337	13 Q9IAZ4	Q9IAZ4 spiroeroides
36	123	20.0	235	6 Q9XSM6	Q9XSM6 saliniri sci
37	120.5	19.6	118	4 Q9UL91	Q9UL91 homo sapien
38	120.5	19.6	118	4 Q9UL72	Q9UL72 homo sapien
39	120.5	19.6	168	4 Q9U056	Q9U056 homo sapien
40	120.5	19.6	210	6 P79336	P79336 felis silve
41	120.5	19.6	246	4 Q9U055	Q9U055 homo sapien
42	120	19.5	147	4 Q9Y509	Q9Y509 homo sapien
43	120	19.5	339	13 Q9IAT8	Q9IAT8 spiroeroides
44	119	19.3	340	13 Q9IAZ0	Q9IAZ0 spiroeroides
45	117.5	19.1	397	4 Q9Y4V0	Q9Y4V0 homo sapien

ALIGNMENTS

RESULT 1
Q9UL85 PRELIMINARY; PRT; 109 AA.
ID Q9UL85
AC Q9UL85;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; Pubmed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035029; AAD56265.1; -
DR HSSP: P01607; 1RET.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1g; 1.
FT NON_TER 109 109
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11761 MW; FBIE43ETC7AFACCC CRC64;

Query Match 86.0%; Score 529; DB 4; Length 109;
Best local similarity 92.7%; Pred. No. 2.5e-47;
Matches 101; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 9 EIVMTQSPATLSVSPGRATLSGRASQSVSNLAWYQKRGQAPRLITYGASTRATGIPA 68
DB I EIVMTQSPATLSVSPGRATLSGRASQSVSNLAWYQKRGQAPRLITYGASTRATGIPA 60
QY 69 RFGSGSGTEFTLTITSSLOSEDAVYVYCOQYNNMPPYFGQTKLEIKR 117
DB 61 RFGSGSGTEFTLTITSSLOSEDAVYVYCOQYNNMPPYFGQTKLEIKR 109

RESULT 2
09UL83 PRELIMINARY: PRT: 108 AA.
AC 09UL83:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035031; AAD56267.1; -
DR HSSP: P01607; 1RET.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.
FT NON_TER 1
FT SEQUENCE 108 AA; 11834 MW; 9P9C5A92EBA96EEA CRC64;

Query Match 83.5%; Score 513.5; DB 4; Length 108;
Best Local Similarity 92.7%; Pred. No. 9, 9e-46;
Matches 101; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY 9 E1YMTGSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 68
DB 1 E1YMTGSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 60
OY 69 RFSGSGSGTEFTLTISLQSEDFAVYVCOQYNNMPPYFGGQTKLEIKR 117
DB 61 RFSGSGSGTEFTLTISLQSEDFAVYVCOQYNNMPPYFGGQTKLEIKR 108

RESULT 3
09UL78 PRELIMINARY: PRT: 109 AA.
AC 09UL78:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -
DR HSSP: P01789; 1MCP.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.
FT NON_TER 1
FT SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EB197 CRC64;

Query Match 73.0%; Score 449; DB 4; Length 109;
Best Local Similarity 82.7%; Pred. No. 4, 4e-39;

Matches 91; Conservative 8; Mismatches 9; Indels 2; Gaps 2;

OY 9 E1YMTGSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 67
DB 1 E1YMTGSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 60
OY 68 RFSGSGSGTEFTLTISLQSEDFAVYVCOQYNNMPPYFGGQTKLEIKR 117
DB 61 RFSGSGSGTEFTLTISLQSEDFAVYVCOQYNNMPPYFGGQTKLEIKR 109

RESULT 4
09UL86 PRELIMINARY: PRT: 109 AA.
AC 09UL86:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035028; AAD56264.1; -
DR HSSP: P01789; 1MCP.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.
FT NON_TER 1
FT SEQUENCE 109 AA; 11928 MW; 2A3325F72C7DAC83 CRC64;

Query Match 70.1%; Score 431; DB 4; Length 109;
Best Local Similarity 79.1%; Pred. No. 3, 2e-37;
Matches 87; Conservative 10; Mismatches 11; Indels 2; Gaps 2;

OY 9 E1YMTGSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 67
DB 1 E1YMTGSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 60
OY 68 RFSGSGSGTEFTLTISLQSEDFAVYVCOQYNNMPPYFGGQTKLEIKR 117
DB 61 RFSGSGSGTEFTLTISLQSEDFAVYVCOQYNNMPPYFGGQTKLEIKR 109

RESULT 5
09UL79 PRELIMINARY: PRT: 108 AA.
AC 09UL79:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).

	Query Match	Similarity	Score	DB	Length
Best Local	61.8%	Pred. No.	3.8e-29		
Matches	68	Conservative	19	Mismatches	20
				Indels	3
				Gaps	2

RESULT	12	
090410		
ID	090410	PRELIMINARY: PRT: 106 AA.
AC	090410;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DE	MONOCLONAL ANTI-IDIOXYPTIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN	
DE	VARIABLE REGION (FRAGMENT).	
OS	Schistosoma japonicum (Blood fluke).	
OC	Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea	
NC	Strioidella; Schistosomatoides; Schistosomatidae; Schistosoma.	
OX	NCBI_TaxID=6182;	
RN	[1]	
RP	SEQUENCE FROM N.A.	

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